

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 02-02-04
Searcher: Beverly C #2528
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site

____ STIC
____ CM-1
____ Pre-S

Type of Search

____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors

____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
☒ Other CGN

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 00:03:08 ; Search time 1498 Seconds
(without alignments)
15874.988 Million cell updates/sec

Title: US-10-005-338B-1

Perfect score: 6525

Sequence: 1 aaatgttgatatttctct.....ttgatcataataagtgaat 6525

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6524	100.0	6525	15	US-10-005-338B-1 Sequence 1, Appli
2	5373.2	82.3	5475	14	US-10-090-458-4 Sequence 4, Appli
3	5255.8	80.5	5463	14	US-10-090-458-1 Sequence 1, Appli
4	5247.4	80.4	5262	10	US-09-971-121-5 Sequence 5, Appli
5	4918.4	75.4	4929	10	US-09-971-121-1 Sequence 1, Appli
6	4807.4	73.7	4917	14	US-10-090-458-3 Sequence 3, Appli
7	4754.8	72.9	4785	10	US-09-971-121-3 Sequence 3, Appli
8	3258.2	49.9	3347	12	US-10-108-260A-160 Sequence 160, App
9	3178	48.7	3268	13	US-10-094-749-984 Sequence 984, App
10	1789.4	27.4	3928	13	US-09-822-846-98 Sequence 98, Appl
11	1731.8	26.5	1943	12	US-10-108-260A-1424 Sequence 1424, Ap
12	1722.8	26.4	1818	15	US-10-204-887-32 Sequence 32, Appl
13	1543.8	23.7	1548	11	US-09-822-846-97 Sequence 97, Appl
14	1182	18.1	1346	9	US-09-962-436-337 Sequence 337, App
15	1182	18.1	1346	10	US-09-880-107-3406 Sequence 3406, Ap

16	1182	18.1	1346	10	US-09-954-531-1033 Sequence 1033, Ap
17	1182	18.1	1346	15	US-10-171-581-333 Sequence 333, App
18	1150.4	17.6	6181	15	US-10-005-338B-4 Sequence 4, Appli
19	1118.8	17.1	5981	15	US-10-005-338B-3 Sequence 3, Appli
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26	894.8	13.7	4798	13	US-10-093-463-197 Sequence 197, App
27	797.4	12.2	5175	12	US-10-085-198-37 Sequence 37, Appli
28	757.4	11.6	974	10	US-09-833-381-1085 Sequence 1085, Ap
29	670.4	10.3	740	12	US-10-242-355-968 Sequence 968, App
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32	600	9.2	668	12	US-10-242-355-970 Sequence 970, App
33	481.8	7.4	2512	12	US-10-108-260A-1795 Sequence 1795, Ap
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41	373.6	5.7	1986	9	US-09-767-870-4 Sequence 4, Appli
42	373.6	5.7	1986	13	US-10-242-568-4 Sequence 4, Appli
43	369.6	5.7	469	10	US-09-880-107-1883 Sequence 1883, Ap
44	319.8	4.9	2007	12	US-10-264-049-708 Sequence 708, App
45	319.2	4.9	1350	10	US-09-833-381-1082 Sequence 1082, Ap

ALIGNMENTS

RESULT 1

US-10-005-338B-1
; Sequence 1, Application US/10005338B
; Publication No. US20030044895A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, Patrice
; APPLICANT: ROSIER-MONTUS, Marie-Francoise
; APPLICANT: PRADES, Catherine
; APPLICANT: ARNOULD-REQUIGNE, Isabelle
; APPLICANT: DUVERGER, Nicolas
; APPLICANT: ALLIEMETS, Rando
; APPLICANT: DEAN, Michael
; TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCA5, ABCA6, ABCA9, AND ABCA10 GENES,
; FILE REFERENCE: ABCA5, 6, 9, 10
; CURRENT APPLICATION NUMBER: US/10/005,338B
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/263,231
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: FR 00403440.1
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4449
; OTHER INFORMATION: n=unknown, may be a o r g o r c o r t
US-10-005-338B-1

Query Match 100.0%; Score 6524; DB 15; Length 6525;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	4141	CAGAGATCATAGATCAAGCTTATCTCAACTTAACTTTTTCAGGCTTTTCCCATCTG	4200
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QY	4201	CATTTGGATTTGGAACAGCTGTTTGTGATATCCCTTATTTTATCAATCTTATTTTGA	4260
DB			
QY	4201	CATTTGGATTTGGAACAGCTGTTTGTGATATCCCTTATTTTATCAATCTTATTTTGA	4260
DB			
QY	4261	TGCTAGGAAGCTTACTGGCAATTTCAATTAATGATTAATTTTATGATTAAGTCTCTG	4320
DB			
QY	4261	TGCTAGGAAGCTTACTGGCAATTTCAATTAATGATTAATTTTATGATTAAGTCTCTG	4320
DB			
QY	4321	CTGTGTTTTTGGCTTATGTTTATGTTCCCATGATTTCTGTTCACTTATATTTGCTT	4380
DB			
QY	4321	CTGTGTTTTTGGCTTATGTTTATGTTCCCATGATTTCTGTTCACTTATATTTGCTT	4380
DB			
QY	4381	CTTTACCTTTTAAAGAAAAATTTTAAATACCAAGAAATTTTGGTCAATTTATCTTCTGTGG	4440

Db 4381 |||||CTTTACCTTTAAAGAAAATTTAAATACCAAGAAATTTGGTCAATTTATCTATCTGTGG 4440
Qy 4441 CAGGTTGNCCTTGATTTGGCAATCACTGAAATACTTTCTTTATGGGATACACAATTTGCAA 4500
Db 4441 CAGGTTGNCCTTGATTTGGCAATCACTGAAATACTTTCTTTATGGGATACACAATTTGCAA 4500
Qy 4501 CTATTTCTTCAATATGCGCTTTGATCATCTCAATCTATCCACTTTCTAGGTTGCTCGA 4560
Db 4501 CTATTTCTTCAATATGCGCTTTGATCATCTCAATCTATCCACTTTCTAGGTTGCTCGA 4560
Qy 4561 TTTCTTTTCAATAAGATTTCTTGGGAAGATGTACGAAAATTTGGACACCTATAATCCAT 4620
Db 4561 TTTCTTTTCAATAAGATTTCTTGGGAAGATGTACGAAAATTTGGACACCTATAATCCAT 4620
Qy 4621 GGGATAGGCTTTCACTAGCTGTTATATCGCTTTACCTGCACTGTACTGTGGATTTTCC 4680
Db 4621 GGGATAGGCTTTCACTAGCTGTTATATCGCTTTACCTGCACTGTACTGTGGATTTTCC 4680
Qy 4681 TCTTACCAATACTATGAGAAAATATGAGGCGAGATCAATAAGAAAAGATCCCTTTTTC 4740
Db 4681 TCTTACCAATACTATGAGAAAATATGAGGCGAGATCAATAAGAAAAGATCCCTTTTTC 4740
Qy 4741 GAAACCTTTCAACGGAAGCTTAAATAATAGGAAGCTTCCAGAACCCACAGACAATGAGGATG 4800
Db 4741 GAAACCTTTCAACGGAAGCTTAAATAATAGGAAGCTTCCAGAACCCACAGACAATGAGGATG 4800
Qy 4801 AAGATGAAGATGTCAAAAGCTGAAAGCTAAAGGCTCAAAAGCTGATGGGTTGCACTGTT 4860
Db 4801 AAGATGAAGATGTCAAAAGCTGAAAGCTAAAGGCTCAAAAGCTGATGGGTTGCACTGTT 4860
Qy 4861 GTGAGGAGAACCACTCAATATGTCAGCAATTTGCAATAAGAAATATGATGACAAGAAAG 4920
Db 4861 GTGAGGAGAACCACTCAATATGTCAGCAATTTGCAATAAGAAATATGATGACAAGAAAG 4920
Qy 4921 ATTTTCTTTTCAAGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTGTGA 4980
Db 4921 ATTTTCTTTTCAAGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTGTGA 4980
Qy 4981 AAAAGAGAGATCTTAGGACTATTTGGTCCAAATGGTCTGCAAAAGCACAATTTATTA 5040
Db 4981 AAAAGAGAGATCTTAGGACTATTTGGTCTCAATGGTCTGCAAAAGCACAATTTATTA 5040
Qy 5041 ATATTTCTGTTGGTGAATTTGAACCAACTTTGAGGCTGATTTTATAGGAGATTTCTT 5100
Db 5041 ATATTTCTGTTGGTGAATTTGAACCAACTTTGAGGCTGATTTTATAGGAGATTTCTT 5100
Qy 5101 CAGAGACAAGTGAAGATGATGATTTCACTGAAGTGTATGGGTTACTGTCTCAGATAAAC 5160
Db 5101 CAGAGACAAGTGAAGATGATGATTTCACTGAAGTGTATGGGTTACTGTCTCAGATAAAC 5160
Qy 5161 CTTTGTGGCCAGATACATACATTTGAGGAAATTTTGAATTTATGGAGCTGTCAAAAGGAA 5220
Db 5161 CTTTGTGGCCAGATACATACATTTGAGGAAATTTTGAATTTATGGAGCTGTCAAAAGGAA 5220
Qy 5221 TGAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5280
Db 5221 TGAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5280
Qy 5281 AACATCTTCAAGAGACTGTAAAGAAATCTACCTGAGGAAATCAAAAGGAAATTTGATTTAAAG 5340
Db 5281 AACATCTTCAAGAGACTGTAAAGAAATCTACCTGAGGAAATCAAAAGGAAATTTGATTTAAAG 5340
Qy 5341 CTCTAAGTATGCTAGGAAATCTCAGATTTACTTTGCTAGATGAACCATCTACAGGATG 5400
Db 5341 CTCTAAGTATGCTAGGAAATCTCAGATTTACTTTGCTAGATGAACCATCTACAGGATG 5400
Qy 5401 ATCCCAAGCCAAACACACATGTGGCGAGCAATTCGAACTGCAATTTAAAGACAGAAAGC 5460
Db 5401 ATCCCAAGCCAAACACACATGTGGCGAGCAATTCGAACTGCAATTTAAAGACAGAAAGC 5460
Qy 5461 GGGCTGCTATTTCTGACCACTCACTATATGAGGAGGCGAGAGGCTGTCTGTGATCGAGTAG 5520

Db 5461 GGGCTGCTATTTCTGACCACTCACTATATGAGGAGGCGAGAGGCTGTCTGTGATCGAGTAG 5520
Qy 5521 CTATCATGCTGTCTGGGCGAGTTAAGATGTATCGGAAACAGTACAAACATCTAAAGAGTAAT 5580
Db 5521 CTATCATGCTGTCTGGGCGAGTTAAGATGTATCGGAAACAGTACAAACATCTAAAGAGTAAT 5580
Qy 5581 TTGGAAGAGGCTACTTTTGGAAAATTTAAATTTGAAAGGCTGATGATAAAGGCTGTAGAGTAG 5640
Db 5581 TTGGAAGAGGCTACTTTTGGAAAATTTAAATTTGAAAGGCTGATGATAAAGGCTGTAGAGTAG 5640
Qy 5641 ACCGCTTCAAGAGAAATTCAGTATATTTTCCAAATGCAAGCGCTCAGGAAAATTTT 5700
Db 5641 ACCGCTTCAAGAGAAATTCAGTATATTTTCCAAATGCAAGCGCTCAGGAAAATTTT 5700
Qy 5701 CTTCTATTTTGGCTTATATAAATTTCTTAAGGAAGATGTTCACTCCCTTTTCAACATCTTTT 5760
Db 5701 CTTCTATTTTGGCTTATATAAATTTCTTAAGGAAGATGTTCACTCCCTTTTCAACATCTTTT 5760
Qy 5761 TTAAGCTGGAAGAGCTAAACATGCTTTTGGCAATTTGAAGAATATAGCTTTTCTCAAGCAA 5820
Db 5761 TTAAGCTGGAAGAGCTAAACATGCTTTTGGCAATTTGAAGAATATAGCTTTTCTCAAGCAA 5820
Qy 5821 CATTTGGAACAGGTTTGTAGAACTCACTAAAGAACAGAGAGGAGAGATTAATAGTTGTG 5880
Db 5821 CATTTGGAACAGGTTTGTAGAACTCACTAAAGAACAGAGAGGAGAGATTAATAGTTGTG 5880
Qy 5881 GAACTTTAAACAGCACACTTTTGGTGGGAAACGAAACAAAGAAAGATAGCTATTTTTC 5940
Db 5881 GAACTTTAAACAGCACACTTTTGGTGGGAAACGAAACAAAGAAAGATAGCTATTTTTC 5940
Qy 5941 TTTGTATTTGTTGGGCTGCTTACTGGGACTTCTTTTCACTTAAATTTTAACTTTTGG 6000
Db 5941 TTTGTATTTGTTGGGCTGCTTACTGGGACTTCTTTTCACTTAAATTTTAACTTTTGG 6000
Qy 6001 TTTAAAAAGTTTATTTGGAATGCTGTAACCTGAGAACCAAGAACGCACTTGAATTTTTC 6060
Db 6001 TTTAAAAAGTTTATTTGGAATGCTGTAACCTGAGAACCAAGAACGCACTTGAATTTTTC 6060
Qy 6061 TAAAGCTCTTAAATGAAATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 6120
Db 6061 TAAAGCTCTTAAATGAAATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 6120
Qy 6121 GTATAAATTAAGTGAAGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 6180
Db 6121 GTATAAATTAAGTGAAGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 6180
Qy 6181 TCATCTTTTCCACCATTCAGAAACAGTCTTCTGAAATTTGTTGTTGTTGTTGTTGTTGTTGTTG 6240
Db 6181 TCATCTTTTCCACCATTCAGAAACAGTCTTCTGAAATTTGTTGTTGTTGTTGTTGTTGTTGTTG 6240
Qy 6241 AGAATAGTTTATTTTAAAGTTTCTTTAAGTTTATGCTTCTTAAATTAAGTACGTA 6300
Db 6241 AGAATAGTTTATTTTAAAGTTTCTTTAAGTTTATGCTTCTTAAATTAAGTACGTA 6300
Qy 6301 ATGTTTCCCAATCTAAATAAAAACTAAATACATAAATAATGCTAGATAAAGGCTACATAAAGC 6360
Db 6301 ATGTTTCCCAATCTAAATAAAAACTAAATACATAAATAATGCTAGATAAAGGCTACATAAAGC 6360
Qy 6361 AATGTGAAGTTTCTTGTCTCTCTTTTAAATTTCTAAAAAGCCACTTTGAAATGGAAAT 6420
Db 6361 AATGTGAAGTTTCTTGTCTCTCTTTTAAATTTCTAAAAAGCCACTTTGAAATGGAAAT 6420
Qy 6421 TGTCTATCCGTAAGCTCAAGTGAAGCACTAGGAAATCTCAATATAGAGATTTTTCAGGAA 6480
Db 6421 TGTCTATCCGTAAGCTCAAGTGAAGCACTAGGAAATCTCAATATAGAGATTTTTCAGGAA 6480
Qy 6481 AGTTATATCCACTAGTGGCAGTCAATTTGATCATATAAAGTGAAT 6525
Db 6481 AGTTATATCCACTAGTGGCAGTCAATTTGATCATATAAAGTGAAT 6525

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; Publication No. US20020123107A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Kilinski, Ligia
; APPLICANT: Le Bihan, Stephane
; TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.403
; CURRENT APPLICATION NUMBER: US/10/090.458
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 25
; OTHER INFORMATION: n = A,T,C or G
US-10-090-458-4

Query Match 82.3%; Score 5373.2; DB 14; Length 5475;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 5375; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	994	AGGTTATTTCAGAAAAATGTCACACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA	1053
Db	97	AGGTTATTTCAGAAAAATGTCACACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA	156
Qy	1054	GAACACTTCTACTGAAGAATTACTTAATAATGCGAGAACCAAAAGAGTAGTGTTCAGG	1113
Db	157	GAACACTTCTACTGAAGAATTACTTAATAATGCGAGAACCAAAAGAGTAGTGTTCAGG	216
Qy	1114	AAATCTTTTCCACTATTTTTTTTATTTTGGTTAATTAATAGCATGATGCATCCAA	1173
Db	217	AAATCTTTTCCACTATTTTTTTTATTTTGGTTAATTAATAGCATGATGCATCCAA	276
Qy	1174	ATAAGAAATATGAAGAAGTGCCTAATAATAGAACTCAATCCTATGCGACAAGTTTACTCTTT	1233
Db	277	ATAAGAAATATGAAGAAGTGCCTAATAATAGAACTCAATCCTATGCGACAAGTTTACTCTTT	336
Qy	1234	CTAATCTAATCTTTGGATATCTCCAGTGACTAATAATTAACAAGCAGCATCATCGAGAAAG	1293
Db	337	CTAATCTAATCTTTGGATATCTCCAGTGACTAATAATTAACAAGCAGCATCATCGAGAAAG	396
Qy	1294	TGCTACTGATCATCTACCTGATGTCAATAATTAAGTAAGTAATACAAATGAAAGAAA	1353
Db	397	TGCTACTGATCATCTACCTGATGTCAATAATTAAGTAAGTAATACAAATGAAAGAAA	456
Qy	1354	TGTTAACATCCAGTCTCTTAAGCCGAGCAACTTTGTAGGTGTGTTTCAAAGACTCCA	1413
Db	457	TGTTAACATCCAGTCTCTTAAGCCGAGCAACTTTGTAGGTGTGTTTCAAAGACTCCA	516
Qy	1414	TGTCCTATGAACCTCGTTTTTCTTGATATGATTCAGATCTCTCTATTAATATGGAAT	1473
Db	517	TGTCCTATGAACCTCGTTTTTCTTGATATGATTCAGATCTCTCTATTAATATGGAAT	576
Qy	1474	CAGAGCTGGCTGTTCAAAATCATGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG	1533
Db	577	CAGAGCTGGCTGTTCAAAATCATGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG	636
Qy	1534	TTTTACAAGCATCATAGATGCTGCCAATTAACAGTTTGAAGACCAATGTTTCTCTTTGGA	1593
Db	637	TTTTACAAGCATCATAGATGCTGCCAATTAACAGTTTGAAGACCAATGTTTCTCTTTGGA	696
Qy	1594	AGGAGCTGGAGTCAACTAAAGCTGTTTATTAATGGGAGAACTGCTGTTGTAGAAATAGATA	1653
Db	697	AGGAGCTGGAGTCAACTAAAGCTGTTTATTAATGGGAGAACTGCTGTTGTAGAAATAGATA	756
Qy	1654	CCTTTCCCGAGGAGTAATTTTAATATACCTAGTATAGCAATTTTCACTTTTGGTACT	1713
Db	757	CCTTTCCCGAGGAGTAATTTTAATATACCTAGTATAGCAATTTTCACTTTTGGTACT	816

Qy	1714	TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAATAAAGAAATTTTTTAAAGATAA	1773
Db	817	TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAATAAAGAAATTTTTTAAAGATAA	876
Qy	1774	TGGGACTTCATGATACCTGCTTTTGGCTTCTCTGGGTTCTTCTATATACAAGTTTAATTT	1833
Db	877	TGGGACTTCATGATACCTGCTTTTGGCTTCTCTGGGTTCTTCTATATACAAGTTTAATTT	936
Qy	1834	TTCTTAATGCTCCCTTCTTATGCGCAGTCATTCGACAGCTTCTTTGGTTATTTCCCTCAAAGTA	1893
Db	937	TTCTTAATGCTCCCTTCTTATGCGCAGTCATTCGACAGCTTCTTTGGTTATTTCCCTCAAAGTA	996
Qy	1894	GCAGCAATGTGATPATTTCTGCTTTTCTTTTATGGATATCATCTGTATTTTTTGTCTT	1953
Db	997	GCAGCAATGTGATPATTTCTGCTTTTCTTTTATGGATATCATCTGTATTTTTTGTCTT	1056
Qy	1954	TAAATGCTGACCTCTTTTAAATAATCAAAACATGTGGATAGTTGAATTTTTTGTGTA	2013
Db	1057	TAAATGCTGACCTCTTTTAAATAATCAAAACATGTGGATAGTTGAATTTTTTGTGTA	1116
Qy	2014	CTGTGGCTTTTGGATTTATTTGGCTTATGATATCTCATAGAAAGTTTTTCCCAATCGT	2073
Db	1117	CTGTGGCTTTTGGATTTATTTGGCTTATGATATCTCATAGAAAGTTTTTCCCAATCGT	1176
Qy	2074	TAGTGTGGCTTTTCACTGCTCTTCTGTCACTGTACTTTTGTGATTTGTCACAGGTCA	2133
Db	1177	TAGTGTGGCTTTTCACTGCTCTTCTGTCACTGTACTTTTGTGATTTGTCACAGGTCA	1236
Qy	2134	TGCATTTAGAAGATTTTAAATGAAGTGTCTTCAATTTCAAATTTGACTCGAGGCCATATC	2193
Db	1237	TGCATTTAGAAGATTTTAAATGAAGTGTCTTCAATTTCAAATTTGACTCGAGGCCATATC	1296
Qy	2194	CTCTAATTAACAATTTATCATCTCACACTTAATAGTAGTATTTCTATGTCTCTTGGCTG	2253
Db	1297	CTCTAATTAACAATTTATCATCTCACACTTAATAGTAGTATTTCTATGTCTCTTGGCTG	1356
Qy	2254	TCATCTTCATCAAGTCAATTCAGGGGAATTTGGCTTAGCGAGATCATCTTTATATTTTC	2313
Db	1357	TCATCTTCATCAAGTCAATTCAGGGGAATTTGGCTTAGCGAGATCATCTTTATATTTTC	1416
Qy	2314	TGAAGCTTCAATTTGGTCAAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGGCAATG	2373
Db	1417	TGAAGCTTCAATTTGGTCAAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGGCAATG	1476
Qy	2374	TTAAATGGAATATTTAGTTTGTAGTGAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGA	2433
Db	1477	TTAAATGGAATATTTAGTTTGTAGTGAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGA	1536
Qy	2434	AAGAAGCCATAAGAAATTTAGTGGTATTTCAAGAAGACATACAGAAAGAGGGTGAAATGTGG	2493
Db	1537	AAGAAGCCATAAGAAATTTAGTGGTATTTCAAGAAGACATACAGAAAGAGGGTGAAATGTGG	1596
Qy	2494	AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAAGTATCTGCTTACTTTGGCC	2553
Db	1597	AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAAGTATCTGCTTACTTTGGCC	1656
Qy	2554	ACAGTGGAAACAGGAAGAGTACATTCATGAATATTTCTTTGTGACCTCTGCCACCTTCTG	2613
Db	1657	ACAGTGGAAACAGGAAGAGTACATTCATGAATATTTCTTTGTGACCTCTGCCACCTTCTG	1716
Qy	2614	ATGGGTTTGCATCTATATATGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA	2673
Db	1717	ATGGGTTTGCATCTATATATGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA	1776
Qy	2674	GAAAAATGATGGCAATTTCTCCACAGTTAGATATACACTTTGATTTTGTGACAGTAGAAG	2733
Db	1777	GAAAAATGATGGCAATTTCTCCACAGTTAGATATACACTTTGATTTTGTGACAGTAGAAG	1836
Qy	2734	AAAAATTTCAATTTTGGCTTCAATCAAAAGGATACACGCCAACATATTAACAAGAG	2793
Db	1837	AAAAATTTCAATTTTGGCTTCAATCAAAAGGATACACGCCAACATATTAACAAGAG	1896

Qy	2794	TGCGAAGGTTTTACTAGATTTAGACATGACAGTATCAAGATAACCAAGCTAAAAAT	2853
Db	1897	TGCGAAGGTTTTACTAGATTTAGACATGACAGTATCAAGATAACCAAGCTAAAAAT	1956
Qy	2854	TAAGTGTGTGTCAAAAAGAAAGCTGTCAATAGGAATGCTGTTCTTGGAAACCAAGA	2913
Db	1957	TAAGTGTGTGTCAAAAAGAAAGCTGTCAATAGGAATGCTGTTCTTGGAAACCAAGA	2016
Qy	2914	TACTGTGCTAGATGACCAACAGCTGGAATGACCCCTGTTCTCGACATATTTGATGA	2973
Db	2017	TACTGTGCTAGATGACCAACAGCTGGAATGACCCCTGTTCTCGACATATTTGATGA	2076
Qy	2974	ATCTTTTAAATAACAGAAAAGCCAAATCGGTGACAGTGTTCAGTACTCAATTTCAATGATG	3033
Db	2077	ATCTTTTAAATAACAGAAAAGCCAAATCGGTGACAGTGTTCAGTACTCAATTTCAATGATG	2136
Qy	3034	AAGCTGACATCTTCTGACAGATGAAAGCTGTGATATCAAGGAATGCTGAAATGTTGTG	3093
Db	2137	AAGCTGACATCTTCTGACAGATGAAAGCTGTGATATCAAGGAATGCTGAAATGTTGTG	2196
Qy	3094	GTTCTTCAATGTTCCCTCAAAAGTAATGCGGATCGGCTACCGCTGAGCATGTACATAG	3153
Db	2197	GTTCTTCAATGTTCCCTCAAAAGTAATGCGGATCGGCTACCGCTGAGCATGTACATAG	2256
Qy	3154	ACAAATATCTGCGCACAGAAATCTTCTTCTCACTGTTAAACAAACATATACCTGGAGCTA	3213
Db	2257	ACAAATATCTGCGCACAGAAATCTTCTTCTCACTGTTAAACAAACATATACCTGGAGCTA	2316
Qy	3214	CTTTATTAACAAGATGACCAACAACTTGTGTATAGTGTGCTTCAAGGACATGGACA	3273
Db	2317	CTTTATTAACAAGATGACCAACAACTTGTGTATAGTGTGCTTCAAGGACATGGACA	2376
Qy	3274	AAATTTTCAGGTTGTTTCTGCCCCCTAGACAGTCAATCAAAATTTGGGTGCTATTCTTATG	3333
Db	2377	AAATTTTCAGGTTGTTTCTGCCCCCTAGACAGTCAATCAAAATTTGGGTGCTATTCTTATG	2436
Qy	3334	GTGTTTCCATGACAGCTTTTGGGAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAAAATG	3393
Db	2437	GTGTTTCCATGACAGCTTTTGGGAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAAAATG	2496
Qy	3394	ACCAAGCAGATTAAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAT	3453
Db	2497	ACCAAGCAGATTAAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAT	2556
Qy	3454	CTTTTGTAGTAATGGAACAGAGCTTACTTATCTTCTGGAACCAAGGCTTCTCTAGTGA	3513
Db	2557	CTTTTGTAGTAATGGAACAGAGCTTACTTATCTTCTGGAACCAAGGCTTCTCTAGTGA	2616
Qy	3514	GCACCATGAGCCTTTGGAAAACACAGATGTATACAAATAGCAAAAGTTTCAATTTTACCT	3573
Db	2617	GCACCATGAGCCTTTGGAAAACACAGATGTATACAAATAGCAAAAGTTTCAATTTTACCT	2676
Qy	3574	TGAAACGTGAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAG	3633
Db	2677	TGAAACGTGAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAG	2736
Qy	3634	TTCCAGATTTTATGTTTTTGGTTCATCAGTCTTTTAAATGCTGTTGCCATCAAC	3693
Db	2737	TTCCAGATTTTATGTTTTTGGTTCATCAGTCTTTTAAATGCTGTTGCCATCAAC	2796
Qy	3694	TTGTTTCCAGACTTATATTTTCTAAACCTGGAGACAAACCAATAAATACAAAACAGTC	3753
Db	2797	TTGTTTCCAGACTTATATTTTCTAAACCTGGAGACAAACCAATAAATACAAAACAGTC	2856
Qy	3754	TGCTTCTTCAAAATTTCTGCTGACTCAGATATCAGTGAATCTTATAGCTTTTTCACAAGCC	3813
Db	2857	TGCTTCTTCAAAATTTCTGCTGACTCAGATATCAGTGAATCTTATAGCTTTTTCACAAGCC	2916
Qy	3814	AGAACATAATGGTGACCATGATTAATGACAGTCAATGATCGGTGGCTCCCATAGTG	3873
Db	2917	AGAACATAATGGTGACCATGATTAATGACAGTCAATGATCGGTGGCTCCCATAGTG	2976
Qy	3874	CGGCTTTAAATGTGATGCAATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAAACAGTA	3933

Db	2977	CGGCTTTAAATGTGATGCAATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAAACAGTA	3036
Qy	3934	CTATGGTTTTTATCTTTACTCTATATTAGTGAATATCATTAGTAACCTACTATCTTTATCAAT	3993
Db	3037	CTATGGTTTTTATCTTTACTCTATATTAGTGAATATCATTAGTAACCTACTATCTTTATCAAT	3096
Qy	3994	TAAATGTGACTGAAACCAATCCAGATCTGGAGTACCCCAATCTTTCAAGAAAATTAATGATA	4053
Db	3097	TAAATGTGACTGAAACCAATCCAGATCTGGAGTACCCCAATCTTTCAAGAAAATTAATGATA	3156
Qy	4054	TAGTTTTTAAATTAAGAGCTGTATTTTCAAGCAGCTTTTCCCTTGGGAATCATTTGTTACTGAA	4113
Db	3157	TAGTTTTTAAATTAAGAGCTGTATTTTCAAGCAGCTTTTCCCTTGGGAATCATTTGTTACTGAA	3216
Qy	4114	TGCCACCTTACTCTTGGCCATGGAATGCAGAGAATCATAAGATCAAAAGCTTATATCTCAAC	4173
Db	3217	TGCCACCTTACTCTTGGCCATGGAATGCAGAGAATCATAAGATCAAAAGCTTATATCTCAAC	3276
Qy	4174	TTAAACTTTTCAAGGCTTTTGGCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCC	4233
Db	3277	TTAAACTTTTCAAGGCTTTTGGCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCC	3336
Qy	4234	CCTTATTTTTTATCATCTTATTTTGTGCTGAGGAGCTTACTGGCATTTTCATTATGGAT	4293
Db	3337	CCTTATTTTTTATCATCTTATTTTGTGCTGAGGAGCTTATTTGGCATTTTCATTATGGAT	3396
Qy	4294	TATATTTTTTATCTGTAAGGTTCCCTGCTGTGTTTTTGGCTTATTTGCTTATTTGTTTCCAT	4353
Db	3397	TATATTTTTTATCTGTAAGGTTCCCTGCTGTGTTTTTGGCTTATTTGCTTATTTGTTTCCAT	3456
Qy	4354	CAGTTATTTCTGTTCACTTATATTGCTTCTTCCACCTTTAAGAAAATTTTAAATACCAAG	4413
Db	3457	CAGTTATTTCTGTTCACTTATATTGCTTCTTCCACCTTTAAGAAAATTTTAAATACCAAG	3516
Qy	4414	AAATTTTGTGCAATTTATCTTCTGTGGCAGCGTGTGTTGTTGTTGCAATCTCACTGAATAA	4473
Db	3517	AAATTTTGTGCAATTTATCTTCTGTGGCAGCGTGTGTTGTTGTTGCAATCTCACTGAATAA	3576
Qy	4474	CTTTCTTTTATGGGATACAAATTCGAATCTTCTTCAATTTGCTTATTTGTTGTTGTTTCCAT	4533
Db	3577	CTTTCTTTTATGGGATACAAATTCGAATCTTCTTCAATTTGCTTATTTGTTGTTGTTTCCAT	3636
Qy	4534	CAATCTATCCACTCTAGGTTGCTGATTTCTTTTCAATAAGATTTCTTTGGAAGATGTAC	4593
Db	3637	CAATCTATCCACTCTAGGTTGCTGATTTCTTTTCAATAAGATTTCTTTGGAAGATGTAC	3696
Qy	4594	GAAAAAATGTGGACACCTTATTAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTT	4653
Db	3697	GAAAAAATGTGGACACCTTATTAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTT	3756
Qy	4654	ACCTGACGTGTACTGTGGATTTTCCCTCTTACATATCTATGAGAAAATAATGAGGCA	4713
Db	3757	ACCTGACGTGTACTGTGGATTTTCCCTCTTACATATCTATGAGAAAATAATGAGGCA	3816
Qy	4714	GATCAATAAGAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAGTCTAAAAATAGGAAGC	4773
Db	3817	GATCAATAAGAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAGTCTAAAAATAGGAAGC	3876
Qy	4774	TTCCAGAAACCAACAGCAATGAGGATGAAGATGTCAAAGCTGAAAGACTTAAAGG	4833
Db	3877	TTCCAGAAACCAACAGCAATGAGGATGAAGATGTCAAAGCTGAAAGACTTAAAGG	3936
Qy	4834	TCAAAAGCTGATGGTTGCCAGTGTGTTGAGGAGAAACCATCCATTTATGTTCAACAAT	4893
Db	3937	TCAAAAGCTGATGGTTGCCAGTGTGTTGAGGAGAAACCATCCATTTATGTTCAACAAT	3996
Qy	4894	TGCATAAAGAAATATGATGACAAAGAAAGATTTTCTTCTTTCAAGAAAAGTAAAGAAAGTGG	4953
Db	3997	TGCATAAAGAAATATGATGACAAAGAAAGATTTTCTTCTTTCAAGAAAAGTAAAGAAAGTGG	4056
Qy	4954	CAACTAAATATCATCTCTTTCTGTGTGTAAGAAAGGAGAGATCTTAGGACTATTTGGGTCCAA	5013

Db 2617 GCACCATGAGCCTTTGGAACAACAGATGTATCAATAGCAAAAGTTTCATTTCTTTACCT 2676
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RESULT 4
US-09-971-121-5
; Sequence 5, Application US/09971121
; Patent No. US20020111477A1
; GENERAL INFORMATION:
; APPLICANT: Nepomichy, Boris
; TITLE OF INVENTION: No. US20020111477A1 Human Transporter Proteins and Polynucleot
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 5262
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-971-121-5

Query Match 80.48; Score 5247.4; DB 10; Length 5262;
Best Local Similarity 99.88; Pred. No. 0;
Matches 5248; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
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937 ATTACATGCAAGTTTACCTGGGCTCGGGTGTGTTGTTGTTTCTTCTTTTAAATAGG 996
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1777 GACTTTCATGATGCTGCTTTTGGCTTTTCTGCTGTTTCTTATATACAAAGTTTAAATTTTTC 1836
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		PRIOR FILING DATE: 2000-10-10			
		; NUMBER OF SEQ ID NOS: 5			
		; SOFTWARE: Fast-Seq for Windows Version 4.0			
		; SEQ ID NO 1			
		; LENGTH: 4929			
		; TYPE: DNA			
		; ORGANISM: homo sapiens			
		US-09-971-121-1			
		Query Match 75.4%; Score 4918.4; DB 10; Length 4929;			
		Best Local Similarity 99.8%; Pred. No. 0;			
		Matches 4919; Conservative 4; Mismatches 6; Indels 0; Gaps 0;			
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Qy	1131	TTTTTTTTTATTTGGTTAAATTAATTAAGTAGCATGATGCATCCAAATAGAAATATGAAGAA	1190		
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Db	181	GTGCCTAATATAGAACTCAATCTCTATGCAAGAAGTTTACTCTTTCTAATCTAAATCTTTGGA	240		
Qy	1251	TATACTCCAGTGACTAATATTAACAAGCAGCATCATGAGAAAGTGTCTACTGATCATCTA	1310		
Db	241	TATACTCCAGTGACTAATATTAACAAGCAGCATCATGAGAAAGTGTCTACTGATCATCTA	300		
Qy	1311	CCTGATGTCATTAATCTGAAGAATATACAAATGAAAAGAAATGTTAAATCCAGTCTC	1370		
Db	301	CCTGATGTCATTAATCTGAAGAATATACAAATGAAAAGAAATGTTAAATCCAGTCTC	360		
Qy	1371	TCTAAGCCGAGCAACTTTGTAGGTGTGTTTCAAGACTCCATGCTCTATGAACCTCGT	1430		
Db	361	TCTAAGCCGAGCAACTTTGTAGGTGTGTTTCAAGACTCCATGCTCTATGAACCTCGT	420		
Qy	1431	TTTTTTTCTGATATGATTCAGATATCTCTATTTATATGGAATCAAGAGCTGGCTGTCA	1490		
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Qy	1491	AAATCATGTGAGGCTGCTCAGTACTGCTCCTCAGTTTCACAGTTTACAGCATCCATA	1550		
Db	481	AAATCATGTGAGGCTGCTCAGTACTGCTCCTCAGTTTCACAGTTTACAGCATCCATA	540		
Qy	1551	GATGCTGCCATTATACAGTTGAGACCAATGTTTCTCTTTGGAGGAGCTGGAGTCAACT	1610		
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Qy	1611	AAAGCTGTTATATGGGAGAACTGCTGTTGTAGAAATAGATACTTTCCCGAGGAGTA	1670		
Db	601	AAAGCTGTTATATGGGAGAACTGCTGTTGTAGAAATAGATACTTTCCCGAGGAGTA	660		
Qy	1671	ATTTTAAATACCTAGTATAGCAATTTTACCTTTTGGATACCTTTTGGCAATTCATATC	1730		
Db	661	ATTTTAAATACCTAGTATAGCAATTTTACCTTTTGGATACCTTTTGGCAATTCATATC	720		
Qy	1731	GTACAGAAAAGAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACT	1790		
Db	721	GTACAGAAAAGAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACT	780		
Qy	1791	GCCTTTTGGCTTTCCCTGGTTCTCTATATACAAAGTTTAAATTTTCTATGCTCCCTCTT	1850		
Db	781	GCCTTTTGGCTTTCCCTGGTTCTCTATATACAAAGTTTAAATTTTCTATGCTCCCTCTT	840		
Qy	1851	ATGCGAGTCATTTGGACAGCTTCTTTGTATTTCTCTCAAGTAGCAGCATTTGATATTT	1910		
Db	841	ATGCGAGTCATTTGGACAGCTTCTTTGTATTTCTCTCAAGTAGCAGCATTTGATATTT	900		
Qy	1911	CTGCTTTTTTTCTTTATGGAATATCATCTGATATTTTTCCTTAAAGTCAACCTCTT	1970		
Db	901	CTGCTTTTTTTCTTTATGGAATATCATCTGATATTTTTCCTTAAAGTCAACCTCTT	960		
Qy	1971	TTTTAAAAATCAAAACATGTGGGAATAGTTGAATTTTTTTGTACTGTGGCTTTTGATTT	2030		
Db	961	TTTTAAAAATCAAAACATGTGGGAATAGTTGAATTTTTTTGTACTGTGGCTTTTGATTT	1020		
Qy	2031	ATTGGGCTTTATGATTAATCTCTATAGAAAGTTTTTCCAAATCGTTAGTGTGGCTTTTCAGT	2090		
Db	1021	ATTGGGCTTTATGATTAATCTCTATAGAAAGTTTTTCCAAATCGTTAGTGTGGCTTTTCAGT	1080		
Qy	2091	CTTTCTGTCACTGTACTTTTGTGATTTGTGATTTGCAAGCTCATGATTTAGAAGATTTT	2150		
Db	1081	CTTTCTGTCACTGTACTTTTGTGATTTGTGATTTGCAAGCTCATGATTTAGAAGATTTT	1140		
Qy	2151	AATGAAGGTGCTTCATTTTCAAAATTTGACTGAGGCCCATATCTCTAATTTATTAACAAT	2210		
Db	1141	AATGAAGGTGCTTCATTTTCAAAATTTGACTGAGGCCCATATCTCTAATTTATTAACAAT	1200		
Qy	2211	ATCATGCTCACACTTAATAGTATATTTCTATGCTCTTGGCTGTCTATCTTGATCAAGTC	2270		
Db	1201	ATCATGCTCACACTTAATAGTATATTTCTATGCTCTTGGCTGTCTATCTTGATCAAGTC	1260		
Qy	2271	ATTCCAGGGGAATTTGGCTTACGAGATCATCTTTATATTTTCTGAAGCCTTCATATGG	2330		
Db	1261	ATTCCAGGGGAATTTGGCTTACGAGATCATCTTTATATTTTCTGAAGCCTTCATATGG	1320		
Qy	2331	TCAAAGGTAAAGAAATTTATGAGGATTTATCAGAGGCAATGTTAATGGAATATATAGT	2390		
Db	1321	TCAAAGGTAAAGAAATTTATGAGGATTTATCAGAGGCAATGTTAATGGAATATATAGT	1380		
Qy	2391	TTTGTAGTAAATTTATCAGGCGAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAAGAAT	2450		
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Qy	2631	TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAATGATGGCAAT	2690		
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Qy	2691	TGTCCACAGTTAGATATACCTTTGTATGTTTGCAGAGTAGAAGAAATTTATCAATTTTG	2750		
Db	1681	TGTCCACAGTTAGATATACCTTTGTATGTTTGCAGAGTAGAAGAAATTTATCAATTTTG	1740		
Qy	2751	GCCTTCAATCAAGGGATACAGCCCAATATATCAAGAGTGCAGAGGTTTTACTA	2810		
Db	1741	GCCTTCAATCAAGGGATACAGCCCAATATATCAAGAGTGCAGAGGTTTTACTA	1800		
Qy	2811	GATTTAGACATGACAGTACTCAAGATATCAAGCTAAAAATTAAGTGGTGGTCAAAAA	2870		
Db	1801	GATTTAGACATGACAGTACTCAAGATATCAAGCTAAAAATTAAGTGGTGGTCAAAAA	1860		
Qy	2871	AGAAAGCTGCTATTAGGAATGCTGTTTGGGAAACCCAAAGATATCTGCTGTAGTAGAA	2930		
Db	1861	AGAAAGCTGCTATTAGGAATGCTGTTTGGGAAACCCAAAGATATCTGCTGTAGTAGAA	1920		
Qy	2931	CCAAAGCTGGAATGAGCCCTCTCTCGACATATTTGTATGTAATCTTTTAAATATCAGA	2990		
Db	1921	CCAAAGCTGGAATGAGCCCTCTCTCGACATATTTGTATGTAATCTTTTAAATATCAGA	1980		
Qy	2991	AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTATGATGAAGCTGACATTTCTTGCA	3050		

1981	Db		AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTATGTGATGAAGCTGACTTCTTGCA	2040
3051	Qy		GATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAATGTCTGCTGTTCTTCAATGTTCCCTC	3110
2041	Db		GATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAATGTCTGCTGTTCTTCAATGTTCCCTC	2100
3111	Qy		AAAAGTAAATGGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA	3170
2101	Db		AAAAGTAAATGGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA	2160
3171	Qy		GAATCTCTTTCTTCACTGGTTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAAT	3230
2161	Db		GAATCTCTTTCTTCACTGGTTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAAT	2220
3231	Qy		GACCAACAACTGTGTATAGCTTCCCTTTCAAGGACATGACACAAATTTTTCAGAGTTTGTGTT	3290
2221	Db		GACCAACAACTGTGTATAGCTTCCCTTTCAAGGACATGACACAAATTTTTCAGAGTTTGTGTT	2280
3291	Qy		TCTGCCCTAGACAGTCAATTCAAATTTTGGGTGTCAATTTCTTATGGTGTGTTCCATGACGACT	3350
2281	Db		TCTGCCCTAGACAGTCAATTCAAATTTTGGGTGTCAATTTCTTATGGTGTGTTCCATGACGACT	2340
3351	Qy		TTGGAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAGAGAAATGACCAAGCAGATTTATAGT	3410
2341	Db		TTGGAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAGAGAAATGACCAAGCAGATTTATAGT	2400
3411	Qy		GTATTTACTCAGCGCCACTGGAGGAGAAATGGATTCAAATCTTTTGTGAATGGAA	3470
2401	Db		GTATTTACTCAGCGCCACTGGAGGAGAAATGGATTCAAATCTTTTGTGAATGGAA	2460
3471	Qy		CAGAGCTTACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG	3530
2461	Db		CAGAGCTTACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG	2520
3531	Qy		AAACAAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTTACCTTTGAAAACGTGAAAGTAAA	3590
2521	Db		AAACAAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTTACCTTTGAAAACGTGAAAGTAAA	2580
3591	Qy		TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTT	3650
2581	Db		TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTT	2640
3651	Qy		TTGGTTTCATCACTTTTAAAAATGCTGTGGTTCCTCATCAAACTGTTCACAGACTTATAT	3710
2641	Db		TTGGTTTCATCACTTTTAAAAATGCTGTGGTTCCTCATCAAACTGTTCACAGACTTATAT	2700
3711	Qy		TTTCTAAAACTGGAGACAAACACATAAATACAAAAACAGTCTGCTTCTTCAAAATCTCT	3770
2701	Db		TTTCTAAAACTGGAGACAAACACATAAATACAAAAACAGTCTGCTTCTTCAAAATCTCT	2760
3771	Qy		GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAGCCAGAACATAATGGTGACG	3830
2761	Db		GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAGCCAGAACATAATGGTGACG	2820
3831	Qy		ATGATTAAATGACAGTGACTATGTATCCGTGGCTCCCATAGTCGGCTTTTAAATGTGATG	3890
2821	Db		ATGATTAAATGACAGTGACTATGTATCCGTGGCTCCCATAGTCGGCTTTTAAATGTGATG	2880
3891	Qy		CATTTCAGAAAAGGACTATGTTTTTTCAGAGCTGTTTTCAACAGTACTATGGTTTTATCTTTA	3950
2881	Db		CATTTCAGAAAAGGACTATGTTTTTTCAGAGCTGTTTTCAACAGTACTATGGTTTTATCTTTA	2940
3951	Qy		CCTATATTAGTGAATATCATTTAGTAACTACTATCTTTTATCATTTAAATGTGACTGAACC	4010
2941	Db		CCTATATTAGTGAATATCATTTAGTAACTACTATCTTTTATCATTTAAATGTGACTGAACC	3000
4011	Qy		ATCCAGATCTGGAGTACCCCATCTTTTCAAGAATAATCTGATATAGTTTTTAAAAATTGAG	4070
3001	Db		ATCCAGATCTGGAGTACCCCATCTTTTCAAGAATAATCTGATATAGTTTTTAAAAATTGAG	3060
4071	Qy		CTGTATTTTCAAGCAGCTTTGCTTGGAAATCAITGTTACTGCAATGCCACTTACTTTGCC	4130

Db	3061	CTGTATTTTCAAGCAGCTTTGCTGTGGAATCAATTTGTTACTGCAATGCCACTTACTTTGCC	3121
Qy	4131	ATGGAATAATGCAGAGAATCATAAAGATCAAAAGCTTATATCTCAACTTAAACTTTTCAGGTCCTT	4190
Db	3121	ATGGAATAATGCAGAGAATCATAAAGATCAAAAGCTTAACTCAACTTAAACTTTTCAGGTCCTT	3180
Qy	4191	TTGCCATCTGCATATTTGGATTTGGATTTGGAAGAAGCTGTTGTTGATATCCCTTATTTTTTATCATTT	4250
Db	3181	TTGCCATCTGCATATTTGGATTTGGACAAAGCTGTTGTTGATATCCCTTATTTTTTATCATTT	3240
Qy	4251	CTTATTTTGTATGCTAGGAAGCTTACTTGGCAATTTTCATTATGGAATATATTTTTTATACGTGA	4310
Db	3241	CTTATTTTGTATGCTAGGAAGCTTATTTGGCAATTTTCATTATGGAATATATTTTTTATACGTGA	3300
Qy	4311	AAAGTTCCTGCTGTGGTTTTTTTGGCTTTATTTGGTTATTTGTTCCATCAGTTATTTCTGTTCACT	4370
Db	3301	AAAGTTCCTGCTGTGGTTTTTTTGGCTTTATTTGGTTATTTGTTCCATCAGTTATTTCTGTTCACT	3360
Qy	4371	TATATTTGCTCTTTTACCTTTTAAGAAAAATTTTAAATACCAAAGAAATTTTGGTCATTTATC	4430
Db	3361	TATATTTGCTCTTTTACCTTTTAAGAAAAATTTTAAATACCAAAGAAATTTTGGTCATTTATC	3420
Qy	4431	TATTTCTGTGCGAGGTTGCTGCTTATTTGCAATCACCTGAAATAACTTTCTTTATGCGGATAC	4490
Db	3421	TATTTCTGTGCGAGGTTGCGCTTGTATTTGCAATCACCTGAAATAACTTTCTTTATGCGGATAC	3480
Qy	4491	ACAATTCGAACATATCTTTCAATTATGCTTTTGTATCATCATTCCTCAATCTATCCACTTCTA	4550
Db	3481	ACAATTCGAACATATCTTTCAATTATGCTTTTGTATCATCATTCCTCAATCTATCCACTTCTA	3540
Qy	4551	GGTTGCTCGAATTTCTTTTCAATAAAGATTTCTTGGAAGAATGTACGAAAAATGTGGACACC	4610
Db	3541	GGTTGCTCGAATTTCTTTTCAATAAAGATTTCTTGGAAGAATGTACGAAAAATGTGGACACC	3600
Qy	4611	TATATTCATGAGATAGGCTTTTCAGTAGCTGTTTATATCGCTTATACCTGCGAGTCGTACTG	4670
Db	3601	TATATTCATGAGATAGGCTTTTCAGTAGCTGTTTATATCGCTTATACCTGCGAGTCGTACTG	3660
Qy	4671	TGGATTTTCTCTTTTACAATACTATGAGAAAAAATATGGAGGCGAGATCAATAAGAAAAAGAT	4730
Db	3661	TGGATTTTCTCTTTTACAATACTATGAGAAAAAATATGGAGGCGAGATCAATAAGAAAAAGAT	3720
Qy	4731	CCCTTTTTCAGAAACCTTTTCAACGAAAGTCTAAAAATAGGAAGCTTCCAGAAACCAACAGAC	4790
Db	3721	CCCTTTTTCAGAAACCTTTTCAACGAAAGTCTAAAAATAGGAAGCTTCCAGAAACCAACAGAC	3780
Qy	4791	AATGAGATGAAGATGAGATGTCCTAAAGCTGAAGACTAAAGCTCAAGAGCTGATGGGT	4850
Db	3781	AATGAGATGAAGATGAAGATGTCCTAAAGCTGAAGACTAAAGCTCAAGAGCTGATGGGT	3840
Qy	4851	TGCCAGTGTGTCAGGAGAAACCATCATTTATGGTCAGCAATTTTGCATAAAGAAATATGAT	4910
Db	3841	TGCCAGTGTGTCAGGAGAAACCATCATTTATGGTCAGCAATTTTGCATAAAGAAATATGAT	3900
Qy	4911	GACAAGAAAAGATTTTCTTTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATACATCTCT	4970
Db	3901	GACAAGAAAAGATTTTCTTTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATACATCTCT	3960
Qy	4971	TTCTGTGTGAAAAAAGAGAGATCTTAGGACTATTTGGTCCAAATGGTGTGCGCAAAAGC	5030
Db	3961	TTCTGTGTGAAAAAAGAGAGATCTTAGGACTATTTGGTCCAAATGGTGTGCGCAAAAGC	4020
Qy	5031	ACAATTAATAATTTCTGGTTTGGTGATTTATGAACCAACTTCAGGCCAGGTAATTTTATAGGA	5090
Db	4021	ACAATTAATAATTTCTGGTTTGGTGATTTATGAACCAACTTCAGGCCAGGTAATTTTATAGGA	4080
Qy	5091	GATTTATTTCTTCAGACACAAGTGAAGATGATTTCACTGAAGTGTATGGGTTACTGTCCT	5150
Db	4081	GATTTATTTCTTCAGACACAAGTGAAGATGATTTCACTGAAGTGTATGGGTTACTGTCCT	4140
Qy	5151	CAGATAAACCCCTTTTGGCCGAGATATCTACATTTGCGAGGAACATTTTGAATTTATGGAGCT	5210
Db	4141	CAGATAAACCCCTTTTGGCCGAGATATCTACATTTGCGAGGAACATTTTGAATTTATGGAGCT	4200

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Qy 5211 GTCAAGGAATGAGTCAAGTGCATGAAGAAAGTCAATAGTGAATTAACACATGCACCTT 5270
Db 4201 GTCAAGGAATGAGTCAAGTGCATGAAGAAAGTCAATAGTGAATTAACACATGCACCTT 4260
Qy 5271 GATTAAAGAAATCTTTCAGAGACTGTAAAGAACTACTCGAGGAATCAACAGGAAG 5330
Db 4261 GATTAAAGAAATCTTTCAGAGACTGTAAAGAACTACTCGAGGAATCAACAGGAAG 4320
Qy 5331 TTGTGTTTTCCTTAAGTATGCTAGGGAATCCCTCAGATTAATCTTGTAGATGAACCATCT 5390
Db 4321 TTGTGTTTTCCTTAAGTATGCTAGGGAATCCCTCAGATTAATCTTGTAGATGAACCATCT 4380
Qy 5391 ACAGGTATGATCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTAAA 5450
Db 4381 ACAGGTATGATCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTAAA 4440
Qy 5451 AACAGAAAGCGGCTGCTATTCGACCACTCACTATATGAGGAGGAGAGGCTGTCTGT 5510
Db 4441 AACAGAAAGCGGCTGCTATTCGACCACTCACTATATGAGGAGGAGAGGCTGTCTGT 4500
Qy 5511 GATCGAGTAGCTATCATGTGTCTGGGCACTTAAGATGTATCGGAACAGTACAACTCTA 5570
Db 4501 GATCGAGTAGCTATCATGTGTCTGGGCACTTAAGATGTATCGGAACAGTACAACTCTA 4560
Qy 5571 AAGAGTAAATTTGGAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAC 5630
Db 4561 AAGAGTAAATTTGGAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAC 4620
Qy 5631 CTGAGTAGACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCAAGCGGTGAG 5690
Db 4621 CTGAGTAGACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCAAGCGGTGAG 4680
Qy 5691 GAAAGTTTTCCTCTATTTTGGCTTATAAATTCCTTAAGGAAGTGTTCAGTCCCTTCA 5750
Db 4681 GAAAGTTTTCCTCTATTTTGGCTTATAAATTCCTTAAGGAAGTGTTCAGTCCCTTCA 4740
Qy 5751 CAATCTTTTTTAAGCTGGAAGAGCTTAAACATGCTTTTGCCATTTGAAGAAATATAGCTTT 5810
Db 4741 CAATCTTTTTTAAGCTGGAAGAGCTTAAACATGCTTTTGCCATTTGAAGAAATATAGCTTT 4800
Qy 5811 TCTCAAGCAACATTTGAAGAGGTTTGTGAAGTCTCACTAAAGAAACAGAGGAGGAAGAT 5870
Db 4801 TCTCAAGCAACATTTGAAGAGGTTTGTGAAGTCTCACTAAAGAAACAGAGGAGGAAGAT 4860
Qy 5871 AATAGTTGTGAACCTTTAAACAGACACTTTGTGGGAAACGACACAGAGATAGAGTA 5930
Db 4861 AATAGTTGTGAACCTTTAAACAGACACTTTGTGGGAAACGACACAGAGATAGAGTA 4920
Qy 5931 GTATTTTGA 5939
Db 4921 GTATTTTGA 4929
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RESULT 6

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US-10-090-458-3
; Sequence 3, Application US/10090458
; Publication No. US20020123107A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Kilinski, Ligia
; APPLICANT: Le Bihan, Stephane
; TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.403
; CURRENT APPLICATION NUMBER: US/10/090.458
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4917
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: 2775, 2776
; OTHER INFORMATION: n = A,T,C or G
US-10-090-458-3
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Query Match 73.7%; Score 4807.4; DB 14; Length 4917;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 4891; Conservative 0; Mismatches 7; Indels 50; Gaps 3;

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Qy 1011 ATGTCCACATGCAATTAGGAGGTTAGGAGTTTGAGACAGACAGACACTTCTTACTGAAG 1070
Db 1 ATGTCCACATGCAATTAGGAGGTTAGGAGTTTGAGACAGACAGACACTTCTTACTGAAG 60
Qy 1071 AATTACTTAATTAATGCAAGAACCAAAAAAGAGTAGTGTTCAGGAAATTCCTTTCCACTA 1130
Db 61 AATTACTTAATTAATGCAAGAACCAAAAAAGAGTAGTGTTCAGGAAATTCCTTTCCACTA 120
Qy 1131 TTTTCTTATTTTGGTAAATTAATTAGCATGATGCATCCAAATTAAGAAATATGAAGAA 1190
Db 121 TTTTCTTATTTTGGTAAATTAATTAGCATGATGCATCCAAATTAAGAAATATGAAGAA 180
Qy 1191 GTGCCTTAATAGAACTCAATCTATGGACAAGTTTACTCTTCTAATCTTAATCTTGGGA 1250
Db 181 GTGCCTTAATAGAACTCAATCTATGGACAAGTTTACTCTTCTAATCTTAATCTTGGGA 240
Qy 1251 TATACTCCAGTGAATTAATTAAGAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 1310
Db 241 TATACTCCAGTGAATTAATTAAGAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 300
Qy 1311 CTGTATGTCATTAATTAAGAGAAATATACAATGAAAAAGAAATGTTAATCAATCCAGTCTC 1370
Db 301 CTGTATGTCATTAATTAAGAGAAATATACAATGAAAAAGAAATGTTAATCAATCCAGTCTC 360
Qy 1371 TCTTAAGCCGAGCAACTTTCTAGTGTGTGTTTCAAGAGATCCATGCTTATGAATTCCT 1430
Db 361 TCTTAAGCCGAGCAACTTTCTAGTGTGTGTTTCAAGAGATCCATGCTTATGAATTCCT 420
Qy 1431 TTTTCTCTGATATGATTCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTCTCA 1490
Db 421 TTTTCTCTGATATGATTCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTCTCA 480
Qy 1491 AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGTGTTCACAGTGTTCACAGTCCATCA 1550
Db 481 AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGTGTTCACAGTGTTCACAGTCCATCA 540
Qy 1551 GATGCTGCCATTTATACAGTTGAAGCAATGTTCTCTTTGGAGAGGCTGGAGTCAACT 1610
Db 541 GATGCTGCCATTTATACAGTTGAAGCAATGTTCTCTTTGGAGAGGCTGGAGTCAACT 600
Qy 1611 AAAGCTGTTTATTTAGGAGAACTGCTGTGTAGAAATAGATACCTTTTCCCGAGGAGTA 1670
Db 601 AAAGCTGTTTATTTAGGAGAACTGCTGTGTAGAAATAGATACCTTTTCCCGAGGAGTA 660
Qy 1671 ATTTTAAATACCTAGTTATAGCAATTTTCCCTTTTGGATACCTTTTGGCAATTCATATC 1730
Db 661 ATTTTAAATACCTAGTTATAGCAATTTTCCCTTTTGGATACCTTTTGGCAATTCATATC 720
Qy 1731 GTAGCAGAAAAAGAAAAAATAAAGAAATTTTAAAGATATGAGGACTTCATGATACT 1790
Db 721 GTAGCAGAAAAAGAAAAAATAAAGAAATTTTAAAGATATGAGGACTTCATGATACT 780
Qy 1791 GCCTTTTGGCTTCTCTGGGTTCTTCTATATACAAGTTTAAATTTTCTTATGTCCTTCTT 1850
Db 781 GCCTTTTGGCTTCTCTGGGTTCTTCTATATACAAGTTTAAATTTTCTTATGTCCTTCTT 840
Qy 1851 ATGGCAGTCAATTCGACAGCTTCTTTGTTATTTCTCAAAGTAGCAGCAATTTGATATTT 1910
Db 841 ATGGCAGTCAATTCGACAGCTTCTTTGTTATTTCTCAAAGTAGCAGCAATTTGATATTT 900
Qy 1911 CTGCTTTTTTCTTTTATGATATCATCTGTATTTTTTGTCTTAAATGCTGACACCTCTT 1970
Db 901 CTGCTTTTTTCTTTTATGATATCATCTGTATTTTTTGTCTTAAATGCTGACACCTCTT 960
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Db 3121 AATGCCACCCCTACTCTGCCATGGAAATGCAGAGATCATATA----- 3161
Qy 4172 ACTTAAACTTTTCAGGTCTTTTGGCATCTGCATATTTGGATTGGACAAGCTGTGTGTATAT 4231
Db 3162 -----AGGTCTTTTGGCATCTGCATATTTGGATTGGACAAGCTGTGTGTATAT 3209
Qy 4232 CCCCTTATTTTATCATCTTATTTTGGATCTAGGAAGCTTACTTGGCATTTCAATTATGG 4291
Db 3210 CCCCTTATTTTATCATCTTATTTTGGATCTAGGAAGCTTATTTGGCATTTCAATTATGG 3269
Qy 4292 ATTATATTTTATCTGTAAGTTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTC 4351
Db 3270 ATTATATTTTATCTGTAAGTTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTC 3329
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Qy 4412 AGAATTTTGGTCAATTTATCTTCTGTGGCAGGTTGNCCTTGTATTTGCAATCACTGAAT 4471
Db 3390 AGAATTTTGGTCAATTTATCTTCTGTGGCAGGTTGNCCTTGTATTTGCAATCACTGAAT 3449
Qy 4472 AACTTTCTTTATGGATACACAAATTCCTTTCATATAAGATTTCTTGGAAAGATGT 4531
Db 3450 AACTTTCTTTATGGATACACAAATTCCTTTCATATAAGATTTCTTGGAAAGATGT 3509
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Db 3510 TCCAATCTATCCACTTCTAGTTTGCCTGATTTCTTTCATATAAGATTTCTTGGAAAGATGT 3569
Qy 4592 ACGAAAAATTTGGACACCTTATATCCATGGATAGGCTTTTCACTGTATATCGCC 4651
Db 3570 ACGAAAAATTTGGACACCTTATATCCATGGATAGGCTTTTCACTGTATATCGCC 3629
Qy 4652 TTACTCTGAGTGTACTGTGGATTTTCTTTCATATAAGATTTCTTGGAAAGATGT 4711
Db 3630 TTACTCTGAGTGTACTGTGGATTTTCTTTCATATAAGATTTCTTGGAAAGATGT 3689
Qy 4712 CAGATCAATAAGAAAGATCCCTTTTTCAGAAACCTTTTCAAGAAAGCTTAAATAAGAA 4771
Db 3690 CAGATCAATAAGAAAGATCCCTTTTTCAGAAACCTTTTCAAGAAAGCTTAAATAAGAA 3749
Qy 4772 GCTTCCAGAACCCAGACCAATGAGATGAAGATGTCAAAGCTCAAAGCTCAAAGCTCAA 4831
Db 3750 GCTTCCAGAACCCAGACCAATGAGATGAAGATGTCAAAGCTCAAAGCTCAAAGCTCAA 3809
Qy 4832 GGTCAAAGAGCTGATGGTGGCCAGTGTGTGAGGAGAAACCATTCATTTATGTGAGCAA 4891
Db 3810 GGTCAAAGAGCTGATGGTGGCCAGTGTGTGAGGAGAAACCATTCATTTATGTGAGCAA 3869
Qy 4892 TTTGCATAAAGATATGATGACAAAGAAAGATTTTCTTTCAGAAAGCTTAAAGAAAGT 4951
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Qy 4952 GGCAACTAAATACATCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCC 5011
Db 3930 GGCAACTAAATACATCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCC 3989
Qy 5012 AAATGGTCTGGCAAAAGCAATTTATTAATTTCTGGTGGTGAATTTGAACCACTTC 5071
Db 3990 AAATGGTCTGGCAAAAGCAATTTATTAATTTCTGGTGGTGAATTTGAACCACTTC 4049
Qy 5072 AGGCCAGGTATTTTAGGAGATTTCTTTCAGAGACAAGTGAAGATGATGATTTCACTGAA 5131
Db 4050 AGGCCAGGTATTTTAGGAGATTTCTTTCAGAGACAAGTGAAGATGATGATTTCACTGAA 4109
Qy 5132 GTGTATGGGTACTGTCTCAGATAAACCCCTTTTGTGGCCAGATATCTACATTGCGAGAAC 5191
Db 4110 GTGTATGGGTACTGTCTCAGATAAACCCCTTTTGTGGCCAGATATCTACATTGCGAGAAC 4169
Qy 5192 TTTTGAATTTATGGAGCTGTCAAAGGAATGAGTGAAGTGAATGAAGAAAGTCAATAG 5251
Db 4170 TTTTGAATTTATGGAGCTGTCAAAGGAATGAGTGAAGTGAATGAAGAAAGTCAATAG 4229

Qy 5252 TCGAATAACACATGCACTTTGATTTAAAGAACATCTTTCAGAGACTGTAAAGAAATAC 5311
Db 4230 TCGAATAACACATGCACTTTGATTTAAAGAACATCTTTCAGAGACTGTAAAGAAATAC 4289
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Db 4290 TCGAGAAATCAACAGAAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAT 4349
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Db 4350 TTTGTGTAGATGAACATCTACAGGTATGATCCCAAGCCAAACACACATGTGGCGAGC 4409
Qy 5432 AATTCGAACCTGCAATTTTAAAGAACAGAGCGGTCTGTATTTCTGACCACTCATATATGA 5491
Db 4410 AATTCGAACCTGCAATTTTAAAGAACAGAGCGGTCTGTATTTCTGACCACTCATATATGA 4469
Qy 5492 GAGGCGAGAGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAT 5551
Db 4470 GAGGCGAGAGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAT 4529
Qy 5552 CGGAACAGTACACATCTAAAGAGTAAATTTGGAAGAGGTACTTTTGGAAATTAAT 5611
Db 4530 CGGAACAGTACACATCTAAAGAGTAAATTTGGAAGAGGTACTTTTGGAAATTAAT 4589
Qy 5612 GAAGGACTGGATAGAAACCTAGAGTAGACCGCTTCAAGAGAAATTCAGTATATTTT 5671
Db 4590 GAAGGACTGGATAGAAACCTAGAGTAGACCGCTTCAAGAGAAATTCAGTATATTTT 4649
Qy 5672 CCCAATGCAAGCGTCAAGAAAGTTTCTTCTATTTTGGCTTATAAATTCCTAAGGA 5731
Db 4650 CCCAATGCAAGCGTCAAGAAAGTTTCTTCTATTTTGGCTTATAAATTCCTAAGGA 4709
Qy 5732 AGATGTTCACTCCCTTTCACAACTTTTAAAGCTGGAAGAGCTTAAACATCTTTTGC 5791
Db 4710 AGATGTTCACTCCCTTTCACAACTTTTAAAGCTGGAAGAGCTTAAACATCTTTTGC 4769
Qy 5792 CATTTGAAGATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTGTAGAACTCACTAA 5851
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Db 4890 AACACAGAGATAGATAGTATTTTGA 4917

RESULT 7

US-09-971-121-3
; Sequence 3, Application US/09971121
; Patent No. US20020111477A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; TITLE OF INVENTION: Same
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4785
; TYPE: DNA
; ORGANISM: homo sapiens

US-09-971-121-3

Query Match

72.9%; Score 4754.8; DB 10; Length 4785;

Best Local Similarity 99.8%; Pred. No. 0; Matches 4756; Conservative 4; Mismatches 7; Indels 0; Gaps 0;			
QY	1011	ATGTCCACTGCAATTAGGAGGTTAGGAGTTTGGAGACAGACAGAAACACTTCTACTGAAG	1070
DB	1	ATGTCCACTGCAATTAGGAGGTTAGGAGTTTGGAGACAGACAGAAACACTTCTACTGAAG	60
QY	1071	AATTACTTAATATGACAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA	1130
DB	61	AATTACTTAATATGACAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA	120
QY	1131	TTTTTTTTTATTTGGTTAATAATTAATAGCATGATGCCAATAAGAAATATGAAGAA	1190
DB	121	TTTTTTTTTATTTGGTTAATAATTAATAGCATGATGCCAATAAGAAATATGAAGAA	180
QY	1191	GTSCCTAAATATGAACCTCAATCCTATGGAAGATTTTACTCTTTCTAATCTAATTTCTTTGGA	1250
DB	181	GTSCCTAAATATGAACCTCAATCCTATGGAAGATTTTACTCTTTCTAATCTAATTTCTTTGGA	240
QY	1251	TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA	1310
DB	241	TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA	300
QY	1311	CCTGATGTCATATTAATCTGAAGATATACAATGAAAAAGAAATGTTAAACATCCAGTCTC	1370
DB	301	CCTGATGTCATATTAATCTGAAGATATACAATGAAAAAGAAATGTTAAACATCCAGTCTC	360
QY	1371	TCTAAGCCGAGCAACTTCTGAGTGTGGTTTTTCAAAGACTCCATGCTCTATGAACCTTGGT	1430
DB	361	TCTAAGCCGAGCAACTTCTGAGTGTGGTTTTTCAAAGACTCCATGCTCTATGAACCTTGGT	420
QY	1431	TTTTTTTCTGATATGATCCAGTATCTTCTATATTAATATGGAATTCAGAGCTGGCTGTTC	1490
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QY	1491	AAATCATGTGAGCTGCTCAGTATCTGTCCTCAGGTTTCAAGTTTTTAAGAGATCCATA	1550
DB	481	AAATCATGTGAGCTGCTCAGTATCTGTCCTCAGGTTTCAAGTTTTTAAGAGATCCATA	540
QY	1551	GATGCTGCCATTATACAGTTGGAAGCAATGTTTCTTTGGAAGAGCTGGAGTCAACT	1610
DB	541	GATGCTGCCATTATACAGTTGGAAGCAATGTTTCTTTGGAAGAGCTGGAGTCAACT	600
QY	1611	AAAGCTGTTATTATGGGAGAAACCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTA	1670
DB	601	AAAGCTGTTATTATGGGAGAAACCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTA	660
QY	1671	ATTTTAATATACCTAGTTATAGATTTTCACTTTTGGATACCTTTTGGCAATTCATATC	1730
DB	661	ATTTTAATATACCTAGTTATAGATTTTCACTTTTGGATACCTTTTGGCAATTCATATC	720
QY	1731	GTAGCAGAAAAAGAAAAATTAAGAAATTTTTTAAGATAATGGGACTTCATGATACT	1790
DB	721	GTAGCAGAAAAAGAAAAATTAAGAAATTTTTTAAGATAATGGGACTTCATGATACT	780
QY	1791	GCCTTTTGGCTTTCTCGGGTCTTCTATATACAAGTTTAATTTTTCTTATGCTCCCTCTT	1850
DB	781	GCCTTTTGGCTTTCTCGGGTCTTCTATATACAAGTTTAATTTTTCTTATGCTCCCTCTT	840
QY	1851	ATGGCAGTCAATTCGCA CAGCTTTCTTTGTTATTTTCTCCAAAGTAGCAGCATTTGATATTT	1910
DB	841	ATGGCAGTCAATTCGCA CAGCTTTCTTTGTTATTTTCTCCAAAGTAGCAGCATTTGATATTT	900
QY	1911	CTGCTTTTTTCTTTATAGATATCATCTGTATTTTTTTTGTCTTTAATGCTGCACCTCTT	1970
DB	901	CTGCTTTTTTCTTTATAGATATCATCTGTATTTTTTTTGTCTTTAATGCTGCACCTCTT	960
QY	1971	TTTTAAAAATCAAAACATGTGGGAATAGTTGAAATTTTTTTTGTACTGTGGCTTTTGGATTT	2030
DB	961	TTTTAAAAATCAAAACATGTGGGAATAGTTGAAATTTTTTTTGTACTGTGGCTTTTGGATTT	1020
QY	2031	ATTGGCCTTATGATAATCTCATAGAAAGTTTTCCAAATCGTTAGTGTGGCTTTTCAGT	2090

QY 3171 GAATCTCTTTCTTCACTGGTTAAACAAATATATCTGGAGCTACTTTTATTAACAGAAAT 3230
DB |||||
DB 2161 GAATCTCTTTCTTCACTGGTTAAACAAATATATCTGGAGCTACTTTTATTAACAGAAAT 2220
QY 3231 GACCAACAACTTGATAGCTTGGCTTTCAAGAGCATGACAAATTTTCAGGTGTTGTTT 3290
DB |||||
DB 2221 GACCAACAACTTGATAGCTTGGCTTTCAAGAGCATGACAAATTTTCAGGTGTTGTTT 2280
QY 3291 TCTGCCCTAGACAGCTCAATCAAAATTTGGGTGTCATTTCTTATGGTGTGTTCCATGACGACT 3350
DB |||||
DB 2281 TCTGCCCTAGACAGCTCAATCAAAATTTGGGTGTCATTTCTTATGGGTGTTCCATGACGACT 2340
QY 3351 TTGGAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAGAAATGACCAAGCAGATTAAGT 3410
DB |||||
DB 2341 TTGGAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAGAAATGACCAAGCAGATTAAGT 2400
QY 3411 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGAATCAAAATCTTTTGATGAATGGAA 3470
DB |||||
DB 2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGAATCAAAATCTTTTGATGAATGGAA 2460
QY 3471 CAGAGCTTACTTATTTCTTCTGAAACCAAGCTTCTCTAGTGAGCACCATGAGCCTTTGG 3530
DB |||||
DB 2461 CAGAGCTTACTTATTTCTTCTGAAACCAAGCTTCTCTAGTGAGCACCATGAGCCTTTGG 2520
QY 3531 AAACAAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTTACCTTGAAACCGTGAAAGTAAA 3590
DB |||||
DB 2521 AAACAAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTTACCTTGAAACCGTGAAAGTAAA 2580
QY 3591 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT 3650
DB |||||
DB 2581 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT 2640
QY 3651 TTGTTTCATCACTCTTTTAAATATGCTGCTGCTCCCATCAAACTGCTTCTTTCAAAATTC 3710
DB |||||
DB 2641 TTGTTTCATCACTCTTTTAAATATGCTGCTGCTCCCATCAAACTGCTTCTTTCAAAATTC 2700
QY 3711 TTTCTAAACCTGGAGACAAACACATATAAATAACAAACAAAGTCTGCTTCTTTCAAAATTC 3770
DB |||||
DB 2701 TTTCTAAACCTGGAGACAAACACATATAAATAACAAACAAAGTCTGCTTCTTTCAAAATTC 2760
QY 3771 GCTGACTCAGATATCAGTGTATCTTATAGCTTTTCAAGCAGACAAATTAATGGTGAAG 3830
DB |||||
DB 2761 GCTGACTCAGATATCAGTGTATCTTATAGCTTTTCAAGCAGACAAATTAATGGTGAAG 2820
QY 3831 ATGATTAATCAGAGTACTATGATCCGCTGCTCCCATAGTGGGCTTTAAATGTGATG 3890
DB |||||
DB 2821 ATGATTAATCAGAGTACTATGATCCGCTGCTCCCATAGTGGGCTTTAAATGTGATG 2880
QY 3891 CATTCAGAAAGGACTATGTTTTCAGAGCTGTTTTCACAGTACTATGTTTATCTTTTA 3950
DB |||||
DB 2881 CATTCAGAAAGGACTATGTTTTCAGAGCTGTTTTCACAGTACTATGTTTATCTTTA 2940
QY 3951 CCTATATAGTGAATATCATTAGTAACCTATCTTATCAATTAATTAATGACTGAAC 4010
DB |||||
DB 2941 CCTATATAGTGAATATCATTAGTAACCTATCTTATCAATTAATTAATGACTGAAC 3000
QY 4011 ATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTAATGATATAGTTTAAATTTAG 4070
DB |||||
DB 3001 ATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTAATGATATAGTTTAAATTTAG 3060
QY 4071 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTACTGCAATGCCACCTTACTTTGCC 4130
DB |||||
DB 3061 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTACTGCAATGCCACCTTACTTTGCC 3120
QY 4131 ATGGAATATGAGAGATATCAAGATCAAGCTTTATCTCAACTTAACTTTTCAGGTCTT 4190
DB |||||
DB 3121 ATGGAATATGAGAGATATCAAGATCAAGCTTTATCTCAACTTAACTTTTCAGGTCTT 3180
QY 4191 TTGCCATCTGCATTTGGATTTGACAGCTGTTGTTGATATCCCTTATTTTATTCATT 4250
DB |||||
DB 3181 TTGCCATCTGCATTTGGATTTGACAGCTGTTGTTGATATCCCTTATTTTATTCATT 3240

QY 4251 CTTATTTTGAATGCTAGGAAGCTTACTGGCAATTTCAATATGGATATATTTTATATCTGTA 4310
DB |||||
DB 3241 CTTATTTTGAATGCTAGGAAGCTTACTGGCAATTTCAATATGGATATATTTTATATCTGTA 3300
QY 4311 AAGTTCCCTTGGCTGGTGTGTTTTCCTTATGTTATGTTTCCATCAGTATTTCTGTTCACT 4370
DB |||||
DB 3301 AAGTTCCCTTGGCTGGTGTGTTTTCCTTATGTTATGTTTCCATCAGTATTTCTGTTCACT 3360
QY 4371 TATATTTGCTTTCTTTTCACTTTTAAGAAAAATTTTAAATACCAAGAAATTTTGGTCAATTTATC 4430
DB |||||
DB 3361 TATATTTGCTTTCTTTTCACTTTTAAGAAAAATTTTAAATACCAAGAAATTTTGGTCAATTTATC 3420
QY 4431 TATTTCTGGCAGCGTTGCTTGTATGCAATCACTCACTGAAATTAATCTTTCTTTATGGGATAC 4490
DB |||||
DB 3421 TATTTCTGGCAGCGTTGCTTGTATGCAATCACTGAAATTAATCTTTCTTTATGGGATAC 3480
QY 4491 ACAAATTTGCAACTATTTCTTCAATATGCTTTTGTATCATCTCAATCTATCCACTCTTA 4550
DB |||||
DB 3481 ACAAATTTGCAACTATTTCTTCAATATGCTTTTGTATCATCTCAATCTATCCACTCTTA 3540
QY 4551 GGTGCTGCTGATTTCTTTTCAATAAGATTTCTTGGAGAAATGTACGAAAAATTTGTGCACACC 4610
DB |||||
DB 3541 GGTGCTGCTGATTTCTTTTCAATAAGATTTCTTGGAGAAATGTACGAAAAATTTGTGCACACC 3600
QY 4611 TATAATCCATGGGATAGGCTTTTCACTAGTGTATATCGCTTTTACCTGCACTGTACTG 4670
DB |||||
DB 3601 TATAATCCATGGGATAGGCTTTTCACTAGTGTATATCGCTTTTACCTGCACTGTACTG 3660
QY 4671 TGGATTTTCTCTTACAATACTATGAGAAAAATATGAGGAGCAGATCAATTAAGAAAAAGAT 4730
DB |||||
DB 3661 TGGATTTTCTCTTACAATACTATGAGAAAAATATGAGGAGCAGATCAATTAAGAAAAAGAT 3720
QY 4731 CCCTTTTTCAGAAAACTTTTCAAGAAAGTCTTAAAAATAGGAAGCTTCCAGAACCCACAGAC 4790
DB |||||
DB 3721 CCCTTTTTCAGAAAACTTTTCAAGAAAGTCTTAAAAATAGGAAGCTTCCAGAACCCACAGAC 3780
QY 4791 AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGCTAAAGGTCAAAGAGCTGATGGGT 4850
DB |||||
DB 3781 AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGCTAAAGGTCAAAGAGCTGATGGGT 3840
QY 4851 TGCCAGTGTGTGAGAGAGAAAAATCCATCCATATGCTGAGCAATTTTGATTAAGAAATATGAT 4910
DB |||||
DB 3841 TGCCAGTGTGTGAGAGAGAAAAATCCATCCATATGCTGAGCAATTTTGATTAAGAAATATGAT 3900
QY 4911 GACAGAAAAAGATTTTCTTCTTTCAAGAAAAATGAAGAAAGTGCGCACTAAATACATCTCT 4970
DB |||||
DB 3901 GACAGAAAAAGATTTTCTTCTTTCAAGAAAAATGAAGAAAGTGCGCACTAAATACATCTCT 3960
QY 4971 TTCTGTGTGAAAAAGAGAGAGATCTTTAGGACTATTTGGGTCCAAATGGTGTCTGCAAAAGC 5030
DB |||||
DB 3961 TTCTGTGTGAAAAAGAGAGAGATCTTTAGGACTATTTGGGTCCAAATGGTGTCTGCAAAAGC 4020
QY 5031 ACAAATTTAATATTTCTGTTTGGTGTATTTGAACCAACTTCAGGCCAGGTATTTTATAGGA 5090
DB |||||
DB 4021 ACAAATTTAATATTTCTGTTTGGTGTATTTGAACCAACTTCAGGCCAGGTATTTTATAGGA 4080
QY 5091 GATTAATTTCTCAGAGCAAGTGAAGATGATTTCACTGAAGTGTATGGTGTACTGTCTCT 5150
DB |||||
DB 4081 GATTAATTTCTCAGAGCAAGTGAAGATGATTTCACTGAAGTGTATGGTGTACTGTCTCT 4140
QY 5151 CAGATAAAACCTTTTGTGGCCAGATCTACATTTGCGAGAAACATTTTGAAATTTTATGGAGCT 5210
DB |||||
DB 4141 CAGATAAAACCTTTTGTGGCCAGATCTACATTTGCGAGAAACATTTTGAAATTTTATGGAGCT 4200
QY 5211 GTCAAAAGGAATGAGTGCACAGTGAAGAAAGTCAATAGTGAATTAACATGACATTT 5270
DB |||||
DB 4201 GTCAAAAGGAATGAGTGCACAGTGAAGAAAGTCAATAGTGAATTAACATGACATTT 4260
QY 5271 GATTTTAAAGAACATCTTCAGAGACTGTAAAGAAACTACCTGCGAGATCAAAACGAAG 5330
DB |||||
DB 4261 GATTTTAAAGAACATCTTCAGAGACTGTAAAGAAACTACCTGCGAGATCAAAACGAAG 4320
QY 5331 TTGTGTTTGTCTTAAGTATGCTAGGGAATCTCTCAGATTTACTTTTGCTAGATGAACCATCT 5390

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Db 4321 TTGTGTTTCTCTAAGTAGTCTAGGAATCCTCAGATTACTTTGCTAGTAGAACCATCT 4380
Qy 5391 ACAGGTATGATCCCAAGCAACCAACAGCACATGTGGCGAGCAATTCGAACATGCAATTTAA 5450
Db 4381 ACAGGTATGATCCCAAGCAACCAACAGCACATGTGGCGAGCAATTCGAACATGCAATTTAA 4440
Qy 5451 AACAGAAAGCGGCTGCTATCTTCCACACATCTATATGAGGAGGAGGAGGCTGTCTGT 5510
Db 4441 AACAGAAAGCGGCTGCTATCTTCCACATCTATATGAGGAGGAGGAGGCTGTCTGT 4500
Qy 5511 GATCGAGTAGCTATCATGTGTCTGGCGAGTAAAGATGATCGGAACAGTACAACTATA 5570
Db 4501 GATCGAGTAGCTATCATGTGTCTGGCGAGTAAAGATGATCGGAACAGTACAACTATA 4560
Qy 5571 AAGAGTAAATTTGGAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAC 5630
Db 4561 AAGAGTAAATTTGGAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAC 4620
Qy 5631 CTAGAGTACACCGCTTCAAGAGAAATTCAGTATATTTTCCAAATGCAAGCGCTCAG 5690
Db 4621 CTAGAGTACACCGCTTCAAGAGAAATTCAGTATATTTTCCAAATGCAAGCGCTCAG 4680
Qy 5691 GAAAGTATTTCTCTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTGAGTCCCTTCA 5750
Db 4681 GAAAGTATTTCTCTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTGAGTCCCTTCA 4740
Qy 5751 CAATCTTTTTTAAAGCTGGAAGAGCT 5777
Db 4741 CAATCTTTTTTAAAGCTGGAAGAGGT 4767

RESULT 8
US-10-108-260A-160
; Sequence 160, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cdna
; FILE REFERENCE: HI-A0106
; - CURRENT APPLICATION NUMBER: US/10/108, 260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 160
; LENGTH: 3347
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-160

Query Match 49.9%; Score 3258.2; DB 12; Length 3347;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 3327; Conservative 0; Mismatches 4; Indels 47; Gaps 2;

Qy 2999 TCGGGTCACAGTGTTCAGTACTCATTTTCAGTGAAGTGAAGTCTTTCAGATAGGAA 3058
Db 1 TCGGGTCACAGTGTTCAGTACTCATTTTCAGTGAAGTGAAGTCTTTCAGATAGGAA 60
Qy 3059 AGCTGTGATATCAAGGAATGCTGAATGTTGGTTCCTCAATGTTCTCAAAAGTAA 3118
Db 61 AGCTGTGATATCAAGGAATGCTGAATGTTGGTTCCTCAATGTTCTCAAAAGTAA 120
Qy 3119 ATGGGGATCGGCTACCGCTGAGCATGTATAGACAAATATTTGGCCACAGAACTCT 3178
Db 121 ATGGGGATCGGCTACCGCTGAGCATGTATAGACAAATATTTGGCCACAGAACTCT 180
Qy 3179 TTCTTCACTGGTTAAACAAACATATACCTGGAGCTACTTTTATTAACACAGAAATCACA 3238
Db 181 TTCTTCACTGGTTAAACAAACATATACCTGGAGCTACTTTTATTAACACAGAAATCACA 240
Qy 3239 ACTTGCTATAGCTTGCCTTTCAAGGACATGGAACAAATTTTCAGGTTTGTTCGCCCT 3298
Db 241 ACTTGCTATAGCTTGCCTTTCAAGGACATGGAACAAATTTTCAGGTTTGTTCGCCCT 300
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Qy 3299 AGACAGTCATTCAAATTTGGGTGTCTATTTCTTATGGTGTTCCTATGACGACTTTTGAAGA 3358
Db 301 AGACAGTCATTCAAATTTGGGTGTCTATTTCTTATGGTGTTCCTATGACGACTTTTGAAGA 360
Qy 3359 CGTATTTTAAAGCTAGAGTTGAAGCGAATAATTCACAAGCAGATTTATAGTGTATTTTAC 3418
Db 361 CGTATTTTAAAGCTAGAGTTGAAGCGAATAATTCACAAGCAGATTTATAGTGTATTTTAC 420
Qy 3419 TCAGCAGCCACTGGAGGAGAAATGGATTCAAAATCTTTTGTATGAATTTGGAACACAGCTT 3478
Db 421 TCAGCAGCCACTGGAGGAGAAATGGATTCAAAATCTTTTGTATGAATTTGGAACACAGCTT 480
Qy 3479 ACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCCTTTGGAACAACA 3538
Db 481 ACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCCTTTGGAACAACA 540
Qy 3539 GATGTATACATAGCAAAAGTTTCATTTCTTTTAACTTCTTGAACGTAAGTAATCAGTGAG 3598
Db 541 GATGTATACATAGCAAAAGTTTCATTTCTTTTAACTTCTTGAACGTAAGTAATCAGTGAG 600
Qy 3599 ATCAGTGTGTCTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTCGTTTCA 3658
Db 601 ATCAGTGTGTCTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTCGTTTCA 660
Qy 3659 TCACCTTTTTTAAATGCTGTGGTTCCTCATCAAACTTCTTCCAGACTTATATTTTCTAAA 3718
Db 661 TCACCTTTTTTAAATGCTGTGGTTCCTCATCAAACTTCTTCCAGACTTATATTTTCTAAA 720
Qy 3719 ACCTGGAGACAAACCAATATAAATCAAAAGTGTCTTCTTCAAAATTCGTCT----- 3773
Db 721 ACCTGGAGACAAACCAATATAAATCAAAAGTGTCTTCTTCAAAATTCGTCTGTGTA 780
Qy 3774 -----GACTCAGATATCAGTGATCTTATAGCTTTTTCACAGCCAGACATAA 3822
Db 781 GAGTGTGTAAGACTCAGATATCTGTGATCTTATAGCTTTTTCACAGCCAGACATAA 840
Qy 3823 TGGTGACGATGATTAATGACAGTGTATGTATCGTGGCTCCCATAGTGGCTTTAA 3882
Db 841 TGGTGACGATGATTAATGACAGTGTATGTATCGTGGCTCCCATAGTGGCTTTAA 900
Qy 3883 ATGTGATGATTCAGAAAGGACTATGTTTTCAGAGTGTCTTTCAGAGTACTATGTTT 3942
Db 901 ATGTGATGATTCAGAAAGGACTATGTTTTCAGAGTGTCTTTCAGAGTACTATGTTT 960
Qy 3943 ATTTCTTTACCTATATAGTGAATATCATTAGTAACTATCTATCTTTTCAATTTAAATGTA 4002
Db 961 ATTTCTTTACCTATATAGTGAATATCATTAGTAACTATCTATCTTTTCAATTTAAATGTA 1020
Qy 4003 CTGAAACCATCCAGATCTGGAGTACCCCATTTCTTTTCAAGAAATTAATCTGATATAGTTT 4062
Db 1021 CTGAAACCATCCAGATCTGGAGTACCCCATTTCTTTTCAAGAAATTAATCTGATATAGTTT 1080
Qy 4063 AAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTTCTGCAATGCCACT 4122
Db 1081 AAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTTCTGCAATGCCACT 1140
Qy 4123 ACTTTGCCATGGAATTCAGAGATCATAGATCAAGCTTATATCTCACTTAACTTT 4182
Db 1141 ACTTTGCCATGGAATTCAGAGATCATAGATCAAGCTTATATCTCACTTAACTTT 1170
Qy 4183 CAGGTCTTTTGGCATCTGCATATGGATTTGGAAGCTGTGTGTGATATCCCTTATTTT 4242
Db 1171 -AGGTCTTTTGGCATCTGCATATGGATTTGGAAGCTGTGTGTGATATCCCTTATTTT 1229
Qy 4243 TTATCATTTTATTTTGTAGTGAAGCTTCTGCGATTTCAATTTGATATATTTT 4302
Db 1230 TTATCATTTTATTTTGTAGTGAAGCTTCTGCGATTTCAATTTGATATATTTT 1289
Qy 4303 ATACTGTAAGTTCCTGCTGTGGTTCCTTATTTGCTTATTTGCTTATCTCAGTATATTC 4362
Db 1290 ATACTGTAAGTTCCTGCTGTGGTTCCTTATTTGCTTATTTGCTTATCTCAGTATATTC 1349
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QY	4363	TGTTCACTTATATGCTCTTTTCACTTTAAGAAAAATTTTAAATACCAAGAAATTTGGT	4422
Db	1350	TGTTCACTTATATGCTCTTTTCACTTTAAGAAAAATTTTAAATACCAAGAAATTTGGT	1409
QY	4423	CATTTATCTATCTGTGGCAGCGTGNCTGTGTAATGCAATCACTGAAATTAACCTTCTTTA	4482
Db	1410	CATTTATCTATCTGTGGCAGCGTGGCTGTGTAATGCAATCACTGAAATTAACCTTCTTTA	1469
QY	4483	TGGGATACAAATGCAATCTATCTTCAATATGCTTTTGTATCATCTTCAATCTATC	4542
Db	1470	TGGGATACAAATGCAATCTATCTTCAATATGCTTTTGTATCATCTTCAATCTATC	1529
QY	4543	CACCTCTAGCTGCTGATTTCTTCAATAAGATTTCTTGGAAAGATGTACGAAAAATG	4602
Db	1530	CACCTCTAGCTGCTGATTTCTTCAATAAATTTCTTGGAAAGATGTACGAAAAATG	1589
QY	4603	TGGACACCTATATCAATGGAATAGGCTTTCACTAGCTGTATATGCTTACCTGAGT	4662
Db	1590	TGGACACCTATATCAATGGAATAGGCTTTCACTAGCTGTATATGCTTACCTGAGT	1649
QY	4663	GTGTAATGCTGATTTCTTCAATATCTATGAGAAAAATATGAGGCGAGATCAATAA	4722
Db	1650	GTGTAATGCTGATTTCTTCAATATCTATGAGAAAAATATGAGGCGAGATCAATAA	1709
QY	4723	GAAAAATCCCTTTTTCAGAAACCTTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAAC	4782
Db	1710	GAAAAATCCCTTTTTCAGAAACCTTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAAC	1769
QY	4783	CACGAGCAATGAGGATGAAGATGAAGATGCTGAAAGCTGAAAGCTAAAGGCTCAAGAGC	4842
Db	1770	CACGAGCAATGAGGATGAAGATGAAGATGCTGAAAGCTGAAAGCTAAAGGCTCAAGAGC	1829
QY	4843	TGATGGTTCAGGCTGTGTGAGGAGAAACCATCTATATGTCAGCAATTTGCAATAAG	4902
Db	1830	TGATGGTTCAGGCTGTGTGAGGAGAAACCATCTATATGTCAGCAATTTGCAATAAG	1889
QY	4903	AATATGATGACAAAGAAATTTTCTTCTTCAAGAAAGTAAAGAAAGTGCGCACTAAAT	4962
Db	1890	AATATGATGACAAAGAAATTTTCTTCTTCAAGAAAGTAAAGAAAGTGCGCACTAAAT	1949
QY	4963	ACATCTCTTCTGTGTGAAAAAGGAGAGATCTTTAGGACATTTGGGTCCAAATGGTGCTG	5022
Db	1950	ACATCTCTTCTGTGTGAAAAAGGAGAGATCTTTAGGACATTTGGGTCCAAATGGTGCTG	2009
QY	5023	GCAAAAGCAAAATTAATTAATCTGTGTGAGTGAATTTAGGACATTTGGGTCCAAATGGTGCTG	5082
Db	2010	GCAAAAGCAAAATTAATTAATCTGTGTGAGTGAATTTAGGACATTTGGGTCCAAATGGTGCTG	2069
QY	5083	TTTTAGGAGATTTATCTTCAAGACAAAGTGAAGATGATGATTTCACTCAAGTGTATGGGTT	5142
Db	2070	TTTTAGGAGATTTATCTTCAAGACAAAGTGAAGATGATGATTTCACTCAAGTGTATGGGTT	2129
QY	5143	ACTGTCTCAGATAAACCCTTTGTGGCCAGATCTACATTTGCGAGGAACATTTTGAATTT	5202
Db	2130	ACTGTCTCAGATAAACCCTTTGTGGCCAGATCTACATTTGCGAGGAACATTTTGAATTT	2189
QY	5203	ATGGAGCTGTCAAGGAATGAGTGCAGTCAATGAAAGAGTCAATAGTCCGAATACAC	5262
Db	2190	ATGGAGCTGTCAAGGAATGAGTGCAGTCAATGAAAGAGTCAATAGTCCGAATACAC	2249
QY	5263	ATGCACTTGATTTAAAGAAACATCTTCAAGAGCTGTAAAGAAATCTACCTGCGAGGAATCA	5322
Db	2250	ATGCACTTGATTTAAAGAAACATCTTCAAGAGCTGTAAAGAAATCTACCTGCGAGGAATCA	2309
QY	5323	AACGAAGTGTGTTTGTCTTAAGTATGTAAGGAATCTCAGATTTACTTTGCTAGATG	5382
Db	2310	AACGAAGTGTGTTTGTCTTAAGTATGTAAGGAATCTCAGATTTACTTTGCTAGATG	2369
QY	5383	AACCACTCAAGTATGGATCCCAAGCCAAAACGACATGCTGGCGAGCAATTCGAAGT	5442
Db	2370	AACCACTCAAGTATGGATCCCAAGCCAAAACGACATGCTGGCGAGCAATTCGAAGT	2429
QY	5443	CAITTTAAAAACAGAAAGCGGCTGCTATTCTGACCCTCACTATATGAGGAGGCGAGAG	5502

RESULT 9

US-10-094-749-984
; Sequence 984, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI

Db	2430	CAITTTAAAAACAGAAAGCGGCTGCTATTCTGACCCTCACTATATGAGGAGGCGAGAG	2489
QY	5503	CTGTCTGTGATCGAGTGTAGTATCATGCTGTGCGCAGTTTAAAGTGTATCGGAACAGTAC	5562
Db	2490	CTGTCTGTGATCGAGTGTAGTATCATGCTGTGCGCAGTTTAAAGTGTATCGGAACAGTAC	2549
QY	5563	AACATCTAAAGAGTAAATTTGAAAAAGGCTACTTTTTGAAAAATTAATTTCAAGGAGCTGA	5622
Db	2550	AACATCTAAAGAGTAAATTTGAAAAAGGCTACTTTTTGAAAAATTAATTTCAAGGAGCTGA	2609
QY	5623	TAGAAAACTGAAGTAGACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATTCGAA	5682
Db	2610	TAGAAAACTGAAGTAGACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATTCGAA	2669
QY	5683	GCGCTCAGAGAAATTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCACT	5742
Db	2670	GCGCTCAGAGAAATTTTCTTCTATTTTGGCTATATAAAATTCCTAAGGAAGATGTTCACT	2729
QY	5743	CCCTTTTCACAATCTTTTTTAAAGCTGGAAGAAAGCTAAACATGCTTTTGCCATTTGAAGAAT	5802
Db	2730	CCCTTTTCACAATCTTTTTTAAAGCTGGAAGAAAGCTAAACATGCTTTTGCCATTTGAAGAAT	2789
QY	5803	ATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCTACTAAGAAACAGAGG	5862
Db	2790	ATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCTACTAAGAAACAGAGG	2849
QY	5863	AGGAGATTAATAGTTGTGGAACCTTTTAAACAGCACACTTTTGGTGGGAACGAAACAGAGAG	5922
Db	2850	AGGAGATTAATAGTTGTGGAACCTTTTAAACAGCACACTTTTGGTGGGAACGAAACAGAGAG	2909
QY	5923	ATAGAGTAGTATTGTGAATTTGTTTGGTCTGCTTCTGCTTCTGCTTCTGCTTCTTCTTCTTCT	5982
Db	2910	ATAGAGTAGTATTGTGAATTTGTTTGGTCTGCTTCTGCTTCTGCTTCTGCTTCTTCTTCTTCT	2969
QY	5983	ACTTAATTTTAACTTTTGGTTTAAAAAGTTTTTATTTGGAATGGTAACTGGAGAACCAAGA	6042
Db	2970	ACTTAATTTTAACTTTTGGTTTAAAAAGTTTTTATTTGGAATGGTAACTGGAGAACCAAGA	3029
QY	6043	AGCAGCTTCAAAATTTTCTAAGCTCTTAATTTGAAATGCTGCTGCTGCTGCTGCTGCTTCT	6102
Db	3030	AGCAGCTTCAAAATTTTCTAAGCTCTTAATTTGAAATGCTGCTGCTGCTGCTGCTGCTTCT	3089
QY	6103	TCCTTAAATAAAGATGATGATATAATTAAGTGAAGCTGCAATTTGTATTTGAACTATATTG	6162
Db	3090	TCCTTAAATAAAGATGATGATATAATTAAGTGAAGCTGCAATTTGTATTTGAACTATATTG	3149
QY	6163	AACATATATAGTTGTATGTCATCTTTTTCACCAATTCAGAAACAGTCTTCTGAAATTTGTG	6222
Db	3150	AACATATATAGTTGTATGTCATCTTTTTCACCAATTCAGAAACAGTCTTCTGAAATTTGTG	3209
QY	6223	ATTAAAGAAATTTGAATAGATTTTATTTTAAAGTATCTTTTAAAGTATGCTTCTGAAATTC	6282
Db	3210	ATTAAAGAAATTTGAATAGATTTTATTTTAAAGTATCTTTTAAAGTATGCTTCTGAAATTC	3269
QY	6283	TTCTTAAATAGTACGTAATTTTCCAACTTAAATAAAAAAATAATACATAAATACTTAATGCAT	6342
Db	3270	TTCTTAAATAGTACGTAATTTTCCAACTTAAATAAAAAAATAATACATAAATACTTAATGCAT	3329
QY	6343	AGAAAGATACATAAAGC 6360	
Db	3330	AGAAAGATACATAAAGC 3347	

QY 4749 TCAACGAAGCTCTAAATATAGAAAGCTTCCAGAACCCACGACCAATGAGGATGAAGATGAA 4808
DB 1686 TCAACGAAGCTCTAAATATAGAAAGCTTCCAGAACCCACGACCAATGAGGATGAAGATGAA 1745
QY 4809 GATGCTCAAGCTCAAGACCTAAAGGTCAAGAGCTGATGGTGGCCAGTCTTGTGAGGAG 4868
DB 1746 GATGCTCAAGCTCAAGACCTAAAGGTCAAGAGCTGATGGTGGCCAGTCTTGTGAGGAG 1805
QY 4869 AAACCATCCATATATGCTCAGCAATTTTGCATAAAGAAATATGATGACCAAGAAAGATTTTCTT 4928
DB 1806 AAACCATCCATATATGCTCAGCAATTTTGCATAAAGAAATATGATGACCAAGAAAGATTTTCTT 1865
QY 4929 CTTTCAAGAAAGTAAAGAAAGTGGCAACTAAATATACATCTCTTCTGTGTGAAAGAAAGGA 4988
DB 1866 CTTTCAAGAAAGTAAAGAAAGTGGCAACTAAATATACATCTCTTCTGTGTGAAAGAAAGGA 1925
QY 4989 GAGATCTTAGGACTATTTGGGTCCAAATGGTGGCAAGAGCAATTTATTAATATCTG 5048
DB 1926 GAGATCTTAGGACTATTTGGGTCCAAATGGTGGCAAGAGCAATTTATTAATATCTG 1985
QY 5049 GTTGGTGATATTTGAACCAACTTCAGGCCAGGTATTTTGGAGATTTATTTCTCAGAGACA 5108
DB 1986 GTTGGTGATATTTGAACCAACTTCAGGCCAGGTATTTTGGAGATTTATTTCTCAGAGACA 2045
QY 5109 AGTGAAGATGATGATTCACCTGAAGTGTATGGTCTACTGTCCTCAGATPAAACCCCTTTGTGG 5168
DB 2046 AGTGAAGATGATGATTCACCTGAAGTGTATGGTCTACTGTCCTCAGATPAAACCCCTTTGTGG 2105
QY 5169 CCAGATCACTCATTGCGAGAACATTTTGAATTTATGGAGCTGTCAAAGGAATGAGTGCA 5228
DB 2106 CCAGATCACTCATTGCGAGAACATTTTGAATTTATGGAGCTGTCAAAGGAATGAGTGCA 2165
QY 5229 AGTGACATGAAGAAAGTCATAAGTCGAATTAACATGCACTTGATTTTAAAGAACATCTT 5288
DB 2166 AGTGACATGAAGAAAGTCATAAGTCGAATTAACATGCACTTGATTTTAAAGAACATCTT 2225
QY 5289 CAGAAGCTGTAAAGAAACTCTCTGAGAGAACTCAAGAAAGTGTGTTTGTCTCTAAGT 5348
DB 2226 CAGAAGCTGTAAAGAAACTCTCTGAGAGAACTCAAGAAAGTGTGTTTGTCTCTAAGT 2285
QY 5349 ATGCTAGGGAATCCTCAGATTTACTTTCTAGATGAAACCATCTACAGGTATGGATCCCAA 5408
DB 2286 ATGCTAGGGAATCCTCAGATTTACTTTCTAGATGAAACCATCTACAGGTATGGATCCCAA 2345
QY 5409 GCCAAACAGCACATGTGCGAGCAATTCGAACCTGATTTAAACAGAAAGCGGCTGCT 5468
DB 2346 GCCAAACAGCACATGTGCGAGCAATTCGAACCTGATTTAAACAGAAAGCGGCTGCT 2405
QY 5469 ATTCTGACCACTCACTATATGGAGGAGGAGGCTGTCTGTGATCGAGTAGCTATCATG 5528
DB 2406 ATTCTGACCACTCACTATATGGAGGAGGAGGCTGTCTGTGATCGAGTAGCTATCATG 2465
QY 5529 GTGCTGGGAGTTAAGATGTATCGGAACAGTACCAATCTAAGAGTAAATTTGGAAA 5588
DB 2466 GTGCTGGGAGTTAAGATGTATCGGAACAGTACCAATCTAAGAGTAAATTTGGAAA 2525
QY 5589 GGCTACTTTTTGGAAAATTAATTAAGAGCTGAGTAAACCTAGAAAGTAGACCGCTT 5648
DB 2526 GGCTACTTTTTGGAAAATTAATTAAGAGCTGAGTAAACCTAGAAAGTAGACCGCTT 2585
QY 5649 CAAAGAGAAATTCAGTATATTTTCCAAATGCAAGCGCTCAGGAAAGTTTTTCTTCTATT 5708
DB 2586 CAAAGAGAAATTCAGTATATTTTCCAAATGCAAGCGCTCAGGAAAGTTTTTCTTCTATT 2645
QY 5709 TTGCTTATTAATTTCTTAGGAAGATGTTTCAGTCCCTTTCAATCTTTTTTTTAAAGCTG 5768
DB 2646 TTGCTTATTAATTTCTTAGGAAGATGTTTCAGTCCCTTTCAATCTTTTTTTTAAAGCTG 2705
QY 5769 GAAGAAGCTAAACATGCTTTTGGCATTGAAGATATAGCTTTTCTCAAGCAACATTTGGAA 5828
DB 2706 GAAGAAGCTAAACATGCTTTTGGCATTGAAGATATAGCTTTTCTCAAGCAACATTTGGAA 2765
QY 5829 CAGGTTTTTGTAGAACTCACTAAAGAAACAAGAGGAGGAAGATAATAGTTGTGGAACTTTA 5888

DB 2766 CAGGTTTTTGTAGAACTCACTAAAGAAACAAGAGGAAGATAATAGTTGTGGAACTTTA 2825
QY 5889 AACAGCACACTTTGGTGGGAAACCAACACAAAGAGATAGAGTAGTATTTTGAATTTCTATT 5948
DB 2826 AACAGCACACTTTGGTGGGAAACCAACACAAAGAGATAGAGTAGTATTTTGAATTTCTATT 2885
QY 5949 GTTGGTCTGCTTACTGGGACTTCTTTCTTTTCTTCACTTAATTTTAACTTTGGTTTAAAA 6008
DB 2886 GTTGGTCTGCTTACTGGGACTTCTTTCTTTTCTTCACTTAATTTTAACTTTGGTTTAAAA 2945
QY 6009 GTTTTTATTTGAATGCTTAACCTGGGAAACCAAGAGCACTTGAATTTTCTAAGCTCC 6068
DB 2946 GTTTTTATTTGAATGCTTAACCTGGGAAACCAAGAGCACTTGAATTTTCTAAGCTCC 3005
QY 6069 TTAATTTGAATGCTGTTGGTGTGTTTCTTTTCTTTTCACTTAATTTTAACTTTGGTTTAAAA 6128
DB 3006 TTAATTTGAATGCTGTTGGTGTGTTTCTTTTCTTTTCACTTAATTTTAACTTTGGTTTAAAA 3065
QY 6129 AAGTGAAGCTGATGTTTGTATTTGAAGTATATTTGAACCTATATAGTTTGTATGTCATCTTT 6188
DB 3066 AAGTGAAGCTGATGTTTGTATTTGAAGTATATTTGAACCTATATAGTTTGTATGTCATCTTT 3125
QY 6189 TTCACCAATTCAGAAACAGTGTCTTGAATTTGTGATTTAAAGGAATTTGAATAGATAGT 6248
DB 3126 TTCACCAATTCAGAAACAGTGTCTTGAATTTGTGATTTAAAGGAATTTGAATAGATAGT 3185
QY 6249 TTTATTTTAAAGTATCTTTTAAAGTTTATGCCATCTTCTTAAATAAGTACGTAATGTTTCCA 6308
DB 3186 TTTATTTTAAAGTATCTTTTAAAGTTTATGCCATCTTCTTAAATAAGTACGTAATGTTTCCA 3245
QY 6309 ATCTAAATAAAAACTAATACAT 6331
DB 3246 ATCTAAATAAAAACTAATACAT 3268

RESULT 10

US-09-822-846-98
; Sequence 98, Application US/09822846
; Publication No. US20030027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fectel, Kim
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6400
; CURRENT APPLICATION NUMBER: US/09/822,846
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,605
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 3928
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-846-98

Query Match		27.4%;	Score 1789.4;	DB 11;	Length 3928;
Best Local Similarity		98.2%;	Pred. No. 0;		
Matches 1833;		Conservative 0;	Mismatches 1;	Indels 33;	Gaps 1;
QY	1941	GTATTTTTCCTTTAAATGCTGACACCTCTTTTAAATAATCAAAACATGTGGGAATAGTT	2000		
DB	1	GTATTTTTCCTTTAAATGCTGACACCTCTTTTAAATAATCAAAACATGTGGGAATAGTT	60		
QY	2001	GAATTTTTCCTTTAAATGCTGACACCTCTTTTAAATAATCAAAACATGTGGGAATAGTT	2060		
DB	61	GAATTTTTCCTTTAAATGCTGACACCTCTTTTAAATAATCAAAACATGTGGGAATAGTT	120		
QY	2061	TTTCCCAAAATGCTTTGAGTGGCTTTTCAAGTCCCTTCTGTCACCTGATCTTTTGTGATGTT	2120		
DB	121	TTTCCCAAAATGCTTTGAGTGGCTTTTCAAGTCCCTTCTGTCACCTGATCTTTTGTGATGTT	180		
QY	2121	ATTGCAAGCTCATGCAATTTAGAAATTTTAAATGAAGGTGCTTCAATTTTCAAAATTTGACT	2180		
DB	181	ATTGCAAGCTCATGCAATTTAGAAATTTTAAATGAAGGTGCTTCAATTTTCAAAATTTGACT	240		
QY	2181	GCAGGCCATATCTCTTAATTTATCAATATATCATGCTCACCTTAATAGTATATTTCTAT	2240		
DB	241	GCAGGCCATATCTCTTAATTTATCAATATATCATGCTCACCTTAATAGTATATTTCTAT	300		
QY	2241	GTCTCTTGGCTGCTATCTTGATCAAGTCAATCCAGGGGAATTTGCTTACGGAGATCA	2300		
DB	301	GTCTCTTGGCTGCTATCTTGATCAAGTCAATCCAGGGGAATTTGCTTACGGAGATCA	360		
QY	2301	TCCTTTATTTTCTGAAGCCTTCATATTTGCTCAAGAGTAAAGAAATTTATGAGAGTTA	2360		
DB	361	TCCTTTATTTTCTGAAGCCTTCATATTTGCTCAAGAGTAAAGAAATTTATGAGAGTTA	420		
QY	2361	TCAGAGGCCAATGTTAATGAANAATTAAGTTTATGTAATTAATGAGCCAGTTCTTCA	2420		
DB	421	TCAGAGGCCAATGTTAATGAANAATTAAGTTTATGTAATTAATGAGCCAGTTCTTCA	480		
QY	2421	GAATTTGTAGGAAGAGCCATTAAGAAATTAAGTGGTATTCAGAGACATACAGAAAGAG	2480		
DB	481	GAATTTGTAGGAAGAGCCATTAAGAAATTAAGTGGTATTCAGAGACATACAGAAAGAG	540		
QY	2481	GGTGAATAATGTGAGGCTTTGAGAAATTTGTCATTTGACATATATGAGGGTCAGATTACT	2540		
DB	541	GGTGAATAATGTGAGGCTTTGAGAAATTTGTCATTTGACATATATGAGGGTCAGATTACT	600		
QY	2541	GCCTTACTTGGCCACAGTGGAAACAGGAAGAGTACATTTGATGAATATTTCTTGTGGACTC	2600		
DB	601	GCCTTACTTGGCCACAGTGGAAACAGGAAGAGTACATTTGATGAATATTTCTTGTGGACTC	660		
QY	2601	TGCCCCCTTCTGATGGTTGCTATCTATATATGACACAGCTCTCAGAAATAGATGAA	2660		
DB	661	TGCCCCCTTCTGATGGTTGCTATCTATATATGACACAGCTCTCAGAAATAGATGAA	720		
QY	2661	ATGTTTGAAGCAAGAAATATGATTTGCTTTCCACAGTTAGATATACATTTGATGTT	2720		
DB	721	ATGTTTGAAGCAAGAAATATGATTTGCTTTTCCACAGTTAGATATACATTTGATGTT	780		
QY	2721	TTGACAGTACAGAAATTTATCAATTTTGGCTTTCAATCAAAAGGATACAGCCAAAT	2780		
DB	781	TTGACAGTACAGAAATTTATCAATTTTGGCTTTCAATCAAAAGGATACAGCCAAAT	840		
QY	2781	ATAATACAGAGTGCAGAGGTTTACTAGATTTAGACATGACAGCTATCAAGATAAC	2840		
DB	841	ATAATACAGAGTGCAGAGGTTTACTAGATTTAGACATGACAGCTATCAAGATAAC	900		
QY	2841	CAAGCTAAAAAATTAAGTGGTGGTCAAAAAAGAAAGCTGTCATTAGGAATTTGCTTTCTT	2900		
DB	901	CAAGCTAAAAAATTAAGTGGTGGTCAAAAAAGAAAGCTGTCATTAGGAATTTGCTTTCTT	960		
QY	2901	GGGAACCCAAAGATATCTGCTGTAGATGAACCAACAGCTGGAAATGGAACCCCTTCTCGA	2960		
DB	961	GGGAACCCAAAGATATCTGCTGTAGATGAACCAACAGCTGGAAATGGAACCCCTTCTCGA	1020		

RESULT 11
US-10-108-260A-1424
; Sequence 1424, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cdna
; FILE REFERENCE: HL-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1

QY	2961	CATATTTGATGGAATCTTTTAAATAACAGAAAGCCAAATCGGGTGCAGTGTTCAGTACT	3020
DB	1021	CATATTTGATGGAATCTTTTAAATAACAGAAAGCCAAATCGGGTGCAGTGTTCAGTACT	1080
QY	3021	CATTTTCATGATGAGCTGACATTTCTTGCAGATAGGAAGCTGTGATATCAAGGAATG	3080
DB	1081	CATTTTCATGATGAGCTGACATTTCTTGCAGATAGGAAGCTGTGATATCAAGGAATG	1140
QY	3081	CTGAAATGCTGTTGGTCTTCAATGTTCTCAAAAGTAAATGGGGATCGGCTACCGCTG	3140
DB	1141	CTGAAATGCTGTTGGTCTTCAATGTTCTCAAAAGTAAATGGGGATCGGCTACCGCTG	1200
QY	3141	AGCATGTACATAGACAAATATTTGTCACAGAAATCTCTTTCTTCACTGGTTAAACAAAT	3200
DB	1201	AGCATGTACATAGACAAATATTTGTCACAGAAATCTCTTTCTTCACTGGTTAAACAAAT	1260
QY	3201	ATACCTGGAGCTACTTTATTAACAAGATGACCAACAACTTGTGTATAGCTTGCCTTTC	3260
DB	1261	ATACCTGGAGCTACTTTATTAACAAGATGACCAACAACTTGTGTATAGCTTGCCTTTC	1320
QY	3261	AAGGACATGGACAAATTTTTCAG-----GTTTG	3287
DB	1321	AAGGACATGGACAAATTTTTCAGGAATGCTTGTATAGACAAAGGATGTTATTTGATGTTG	1380
QY	3288	TTTTCTGCCCTAGACAGTCAATTTCAAAATTTGGGTGTCTTTCTTATGGTGTTCATGACG	3347
DB	1381	TTTTCTGCCCTAGACAGTCAATTTCAAAATTTGGGTGTCTTTCTTATGGTGTTCATGACG	1440
QY	3348	ACTTTTGAAGACGTAATTTTAAAGCTAGAAAGTTGAGCAGAAATTTGACCAAGCAGATAT	3407
DB	1441	ACTTTTGAAGACGTAATTTTAAAGCTAGAAAGTTGAGCAGAAATTTGACCAAGCAGATAT	1500
QY	3408	AGTGTATTTTACTCAGCAGCCACTGGAGGAGAAATGGAATTCAAATCTTTTGTGATAATG	3467
DB	1501	AGTGTATTTTACTCAGCAGCCACTGGAGGAGAAATGGAATTCAAATCTTTTGTGATAATG	1560
QY	3468	GAACAGAGCTTACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTT	3527
DB	1561	GAACAGAGCTTACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTT	1620
QY	3528	TGGAACCAACAGATGATACAAATAGCAAAAGTTTCAATTTCTTCTTACCTTGAACGTAAGT	3587
DB	1621	TGGAACCAACAGATGATACAAATAGCAAAAGTTTCAATTTCTTCTTACCTTGAACGTAAGT	1680
QY	3588	AAATCAGTGAGATCAGTCTCTCTCTCTTAAATTTTCTTCAAGATTCAGATTTTATG	3647
DB	1681	AAATCAGTGAGATCAGTCTCTCTCTCTTAAATTTTCTTCAAGATTCAGATTTTATG	1740
QY	3648	TTTTTGGTTCATCACTCTTTTAAATAATGCTGTGGTTCCCATCAAACTTTGTTCCAGACTTA	3707
DB	1741	TTTTTGGTTCATCACTCTTTTAAATAATGCTGTGGTTCCCATCAAACTTTGTTCCAGACTTA	1800
QY	3708	TATTTTCTTAAACCTGGAGACAAACCAATATAAATAAATAAAGTCTGCTTCTTCAAAAT	3767
DB	1801	TATTTTCTTAAACCTGGAGACAAACCAATATAAATAAATAAAGTCTGCTTCTTCAAAAT	1860
QY	3768	TCGCTG 3774	
DB	1861	TCGCTG 1867	

; SEQ ID NO 1424

; LENGTH: 1943

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-108-260A-1424

Query Match. 26.5%; Score 1731.8; DB 12; Length 1943;

Best local similarity 99.9%; Pred. No. 0;

Matches 1733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAATGTTGATATTTCTCTAGCAGGCTGTCACAGGTTAGTTCAGGTCATAGTTT 60
DB 209 AAAATGTTGATATTTCTCTAGCAGGCTGTCACAGGTTAGTTCAGGTCATAGTTT 268
QY 61 CTACCCACATTTCTTGAACGTAGTCTGTCATTTTAGTTTATTTTCAAAAACTTTTGCAG 120
DB 269 CTACCCACATTTCTTGAACGTAGTCTGTCATTTTAGTTTATTTTCAAAAACTTTTGCAG 328
QY 121 TACCTTTTGGTCTGTCCTTGTGTGCTTGCAGTGAACAGTCTGGATTGGACAGTGT 180
DB 329 TACCTTTTGGTCTGTCCTGTCGTGCTTGCAGTGAACAGTCTGGATTGGACAGTGT 388
QY 181 CTGTCCTTAGTTCAGTTTCTCAAGCCTTTGTCACTAATAGATTGGATTATGTATG 240
DB 389 CTGTCCTTAGTTCAGTTTCTCAAGCCTTTGTCACTAATAGATTGGATTATGTATG 448
QY 241 TCCAGCTTGGGAATTATTACAGGAATTAATAAACAACCTTTTGTAGTCTCTTCTTGAGCTC 300
DB 449 TCCAGCTTGGGAATTATTACAGGAATTAATAAACAACCTTTTGTAGTCTCTTCTTGAGCTC 508
QY 301 TCTTCTATTGTTTCCCTCTTACTTTTGTCTTCCCTGTGGCTGTCTTCTATCTCTC 360
DB 509 TCTTCTATTGTTTCCCTCTTACTTTTGTCTTCCCTGTGGCTGTCTTCTATCTCTC 568
QY 361 AGCCAGAGCTAGTGTATTTTCTCCATGTGTGTACACATTTGTGCGAGTGCACAC 420
DB 569 AGCCAGAGCTAGTGTATTTTCTCCATGTGTGTACACATTTGTGCGAGTGCACAC 628
QY 421 CATATCCAGGCCCAATGTTAGGAGTGTAGAGAAAGCAAGGATTTGGCTCATCC 480
DB 629 CATATCCAGGCCCAATGTTAGGAGTGTAGAGAAAGCAAGGATTTGGCTCATCC 688
QY 481 TCTTCAACGATAGTCTCCATTTGAATAGAGAAAGGTTTCTTCCCTCAGAGTGTGGCT 540
DB 689 TCTTCAACGATAGTCTCCATTTGAATAGAGAAAGGTTTCTTCCCTCAGAGTGTGGCT 748
QY 541 GCATAGGCTTTGTTACTGTAGTCTGGCCCTGTACCATGGGATTTGCTTGCATGTGGG 600
DB 749 GCATAGGCTTTGTTACTGTAGTCTGGCCCTGTACCATGGGATTTGCTTGCATGTGGG 808
QY 601 ATACAGAGAAATTCAGAAAAGAAAAGATTTGCTATTTCTACATTTCCCTGAGCAT 660
DB 809 ATACAGAGAAATTCAGAAAAGAAAAGATTTGCTATTTCTACATTTCCCTGAGCAT 868
QY 661 AAGACCTCCCTTGCCCATTTCTCAATTTCAAGCTTAAGGCTTTCTTCTGAGCTGCTCTGT 720
DB 869 AAGACCTCCCTTGCCCATTTCTCAATTTCAAGCTTAAGGCTTTCTTCTGAGCTGCTCTGT 928
QY 721 GGGCGGTTGGGAGATACCAAGAGAAAAGTACCACTGTGTATATGTTGGTATTTCAA 780
DB 929 GGGCGGTTGGGAGATACCAAGAGAAAAGTACCACTGTGTATATGTTGGTATTTCAA 988
QY 781 ATTCTGCTCTACCTATTTTACATGCTTGTATTTTCTTCTTCTGAGCTGACAGATTGCTCT 840
DB 989 ATTCTGCTCTACCTATTTTACATGCTTGTATTTTCTTCTTCTGAGCTGACAGATTGCTCT 1048
QY 841 CCATGCTATTTCTGCTCAGTTTCTTAAGAGACAGCTTTGGAGTATGCTTTAATCCATCTTAC 900
DB 1049 CCATGCTATTTCTGCTCAGTTTCTTAAGAGACAGCTTTGGAGTATGCTTTAATCCATCTTAC 1108
QY 901 CTGGGACTGAACAGCTGCTTATTTTCCGTTAAAAATTACATGCACTTTTACTGCGTGGC 960
DB 1109 CTGGGACTGAACAGCTGCTTATTTTCCGTTAAAAATTACATGCACTTTTACTGCGTGGC 1168

QY 961 TCCGGGTTGTTGTTGTTGTTTCTTCTTAAATAGTATTTTATTCAGAAAAATGTCACCTG 1020
DB 1169 TCCGGGTTGTTGTTGTTGTTTCTTCTTAAATAGTATTTTATTCAGAAAAATGTCACCTG 1228
QY 1021 CAATTAGGAGGTAGGAGTTTGGAGACAGACAGAACACTTCTTCTAGTGAAGAATTACTTAA 1080
DB 1229 CAATTAGGAGGTAGGAGTTTGGAGACAGACAGAACACTTCTTCTAGTGAAGAATTACTTAA 1288
QY 1081 TTAATATGCAGAACCAAAAGAGTAGTGTTCAGAAATTCCTTTTCCACTATTTTAT 1140
DB 1289 TTAATATGCAGAACCAAAAGAGTAGTGTTCAGAAATTCCTTTTCCACTATTTTAT 1348
QY 1141 TTTGGTTAATATTAAATAGCATGTCATCCAAATAAGAAATATGAAGAAGTGCCTAATA 1200
DB 1349 TTTGGTTAATATTAAATAGCATGTCATCCAAATAAGAAATATGAAGAAGTGCCTAATA 1408
QY 1201 TAGAACTCAATCCTATGGACAAGTTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
DB 1409 TAGAACTCAATCCTATGGACAAGTTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1468
QY 1261 TGAATAATATTCAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTTACCTGATGTCA 1320
DB 1469 TGAATAATATTCAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTTACCTGATGTCA 1528
QY 1321 TAAATTAAGAAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTCTCTTAAGCCGA 1380
DB 1529 TAAATTAAGAAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTCTCTTAAGCCGA 1588
QY 1381 GCAACTTTGTAGTGTGGTTTCAAGACTTCAATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1440
DB 1589 GCAACTTTGTAGTGTGGTTTCAAGACTTCAATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1648
QY 1441 ATATGATTTCCAGTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1500
DB 1649 ATATGATTTCCAGTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1708
QY 1501 AGGCTCTCAGTACTGCTCTCAGGTTTCAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1560
DB 1709 AGGCTCTCAGTACTGCTCTCAGGTTTCAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1768
QY 1561 TTATACAGTTGAAGACCAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1620
DB 1769 TTATACAGTTGAAGACCAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1828
QY 1621 TTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTAAATTTTAAAT 1680
DB 1829 TTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTAAATTTTAAAT 1888
QY 1681 ACCTAGTTATAGCAATTTTCACTTTTGGATATCTTTTGGCAATTCATATCGTAGC 1735
DB 1889 ACCTAGTTATAGCAATTTTCACTTTTGGATATCTTTTGGCAATTCATATCGTAGC 1943

RESULT 12

US-10-204-887-32

; Sequence 32, Application US/10204887

; Publication No. US20030124569A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: PANZER, Scott R.

; APPLICANT: SPIRO, Peter A.

; APPLICANT: BANVILLE, Steven C.

; APPLICANT: SHAH, Purvi

; APPLICANT: CHALUP, Michael S.

; APPLICANT: CHEN, Alice

; APPLICANT: D'SA, Steven A.

; APPLICANT: ANSHEY, Stefan

; APPLICANT: DAHL, Christopher R.

; APPLICANT: DAM, Tam C.

; APPLICANT: DANIELS, Susan E.

; APPLICANT: DUFOUR, Gerard E.

APPLICANT: FLORES, Vincent
APPLICANT: FONG, Willy T.
APPLICANT: GREENAWALT, Lila B.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: JONES, Anissa L.
APPLICANT: LIU, Tommy F.
APPLICANT: ROSEBERRY, Ann M.
APPLICANT: ROSEN, Bruce H.
APPLICANT: RUSSO, Frank D.
APPLICANT: STOCKREHER, Theresa K.
APPLICANT: DAPFO, Abel
APPLICANT: WRIGHT, Rachel J.
APPLICANT: YAP, Pierre E.
APPLICANT: YU, Jimmy Y.
APPLICANT: BRADLEY, Diana L.
APPLICANT: BRATCHER, Shawn R.
APPLICANT: CHEN, Wensheng
APPLICANT: COHEN, Howard J.
APPLICANT: HODGSON, David M.
APPLICANT: LINCOLN, Stephen E.
TITLE OF INVENTION: SECRETORY MOLECULES
FILE REFERENCE: PT-1134 PCT
CURRENT APPLICATION NUMBER: US/10/204,887
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: 60/185,215; 60/185,216; 60/205,232; 60/205,323; 60/205,287;
60/205,324; 60/205,286
PRIOR FILING DATE: 2000-02-24; 2000-02-24; 2000-05-16; 2000-05-17; 2000-05-17;
2000-05-17; 2000-05-17
NUMBER OF SEQ ID NOS: 159
SOFTWARE: PERL Program
SEQ ID NO 32
LENGTH: 1818
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030124569A1 LI:445188.1:2000MAY01
US-10-204-887-32

Query Match 26.4%; Score 1722.8; DB 15; Length 1818;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1735; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 AAAATGTTGATATTTCTCTAGCAGGCTGTCACACAGGTTAGGTTGAGGTCATAGATTT 60
Db 81 AAAATGTTGATATTTCTCTAGCAGGCTGTCACACAGGTTAGGTTGAGGTCATAGATTT 140

Qy 61 CTACCCACATTTCTTGAAGTGTAGTGTCTCATTTTGTATTTTCAAAAACCTTTTGAC 120
Db 141 CTACCCACATTTCTTGAAGTGTAGTGTCTCATTTTGTATTTTCAAAAACCTTTTGAC 200

Qy 121 TACCTTTTGGTCTGTCTGTGTGTGCTGCTGAGTGAACAGTCTGGAATTTGACAGTGT 180
Db 201 TACCTTTTGGTCTGTCTGTGTGTGCTGCTGAGTGAACAGTCTGGAATTTGACAGTGT 260

Qy 181 CTGTCTGTAGTTGAGTTTCTCAAGCCTTGTGACACTATAGATTTGGAATTTATGTATG 240
Db 261 CTGTCTGTAGTTGAGTTTCTCAAGCCTTGTGACACTATAGATTTGGAATTTATGTATG 320

Qy 241 TCACAGCTTGGGAATTTATACAGGAATTAATAAACAACCTTTTATAGAGTCTTTTCTGAGCTC 300
Db 321 TCACAGCTTGGGAATTTATACAGGAATTAATAAACAACCTTTTATAGAGTCTTTTCTGAGCTC 380

Qy 301 TCTTTCTATTTGTTCCCTTCTACTTTTGTCTTCCCTGCTGGCTGTGTTTCTATCTCC 360
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Qy 361 AGCCAGAGCTAGTGTATTTCTCCATTTGTTTACACACTTGTGACGCTGCAACCCAC 420
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Qy 421 CATATCCAGGCCCCAATGGTAGGAGGTAGAGAAAGCAAAAGGAGTTGGCTCATCC 480
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Db 501 CATATCCAGGGCCCCAATGGTAGGAGGTAGAGAAAGCAAAAGGGATTGGCCCTCATCC 560
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Db 681 ATACAGGAGATTTAGAAAGAAAGATTTGCTATTTCTACATTTCCCTCCAGCATTT 740
Qy 661 AAGACCTCCCTTGGCCCATTTCCATTTCAAAAGCTAAGGCTTCTTTCTGGAGCTGCTCTCT 720
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Db 861 ATTCTGGTCTACCTTATTTTACATGCTTGTATTTTCTTTTTCAGAGCTGACAGATTTGCTCT 920
Qy 841 CCATGCTTCTGTCAGTTTCTTAAAGAGAGACAGCTTGGAGTATGCTTAAATCCATCTTAC 900
Db 921 CCATGCTTCTGTCAGTTTCTTAAAGAGAGACAGCTTGGAGTATGCTTAAATCCATCTTAC 980
Qy 901 CTGGGACTGAAACAGCTGCTTATTTTGGCGTTTAAATAATTTACATGCAAGTTTACTGCGTGGC 960
Db 981 CTGGGACTGAAACAGCTGCTTATTTTGGCGTTTAAATAATTTACATGCAAGTTTACTGCGTGGC 1040
Qy 961 TCCGGGTTTGTGTTGTTGTTTCTCT - CTTAAATAGGTTTATTTTCAAGAAACATGCTCAT 1019
Db 1041 TCCGGGTTTGTGTTGTTGTTTCTCTCTTAAATAGGTTTATTTTCAAGAAACATGCTCAT 1100
Qy 1020 GCAATTTAGGAGGTAGGAGTTTGGAGACAGACACAGCACTTCTACTGAAGAAATTTACTTTA 1079
Db 1101 GCAATTTAGGAGGTAGGAGTTTGGAGACAGACACAGCACTTCTACTGAAGAAATTTACTTTA 1160
Qy 1080 ATTTAAATGAGAACCAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTATTTTCTTTT 1139
Db 1161 ATTTAAATGAGAACCAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTATTTTCTTTT 1220
Qy 1140 TTTTGGTTAATTAATTTAGCATGATGCATCCAAATAGAAATATAGAAAGTGGCTAT 1199
Db 1221 TTTTGGTTAATTAATTTAGCATGATGCATCCAAATAGAAATATAGAAAGTGGCTAT 1280
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Qy 1260 GTGACTAATATTATACAGCAGCATCATGAGAAAGTGTCTACTGATCATCTCTGATGTC 1319
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RESULT 13
US-09-822-846-97
; Sequence 97, Application US/09822846
; Publication No. US20030027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulkota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6400
; CURRENT APPLICATION NUMBER: US/09/822,846
; CURRENT FILING DATE: 2001-03-29
; PRIOR FILING DATE: 60/195,605
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-846-97

Query Match 23.7%; Score 1543.8; DB 11; Length 1548;
Best Local Similarity 99.8%; Pred. No. 1.3e-309;
Matches 1545; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3386 AGAAATTGACCAACGATATAGTGTATTTACTCAGCAGCCACTGCGAGGAAGAAATGGA 3445
Db 1 AGAAATTGACCAACGATATAGTGTATTTACTCAGCAGCCACTGCGAGGAAGAAATGGA 60
Qy 3446 TTCAAAATCTTTTGATGAAATGGAACAGAGCTTACTTTCTTCTGAAACCAAGGCTTC 3505
Db 61 TTCAAAATCTTTTGATGAAATGGAACAGAGCTTACTTTCTTCTGAAACCAAGGCTTC 120
Qy 3506 TCTAGTGAGCAGCAATGAGCCTTTGGAAACACAGATGTATACATAGCAAAAGTTTCATTT 3565
Db 121 TCTAGTGAGCAGCAATGAGCCTTTGGAAACACAGATGTATACATAGCAAAAGTTTCATTT 180
Qy 3566 CTTTACCTTGAACGTAAGTAATCAGTGAGATCAGTGTCTGCTCTCTTTTAATTTT 3625
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Qy 3986 TTTATCAATTAATGCTGACTGAAACCAATCCAGATCTGGAGTACCCCAATTTCTTCAAGAAAT 4045
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Qy 4106 TACTGCAATGCCACCTTACTTTTGCCATGGAAATGCAGAAATCATAAGATCAAAAGCTTA 4165
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Qy 4166 TACTCAACTTAACTTTTCAAGTCTTTTGGCATCTGCATATTTGATTTGGACAAGCTGTTGT 4225
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Qy 4346 TGTTCATCAGTTTATCTGTTCACTTTATATTTGCTTCTTTTCACTTTTAAAGAAATTTTAA 4405
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Qy 4406 TACCAAGAAATTTTGGTCACTTTATCTTCTGCGCAGCGTTGCTTGTATTTGCAATCAC 4465
Db 1021 TACCAAGAAATTTTGGTCACTTTATCTTCTGCGCAGCGTTGCTTGTATTTGCAATCAC 1080
Qy 4466 TGAATAAATCTTTTATGGGATACAAATTTGCAACTTCTTCAATTTGCTTGTAT 4525
Db 1081 TGAATAAATCTTTTATGGGATACAAATTTGCAACTTCTTCAATTTGCTTGTAT 1140
Qy 4526 CATCATTTCCAAATCTATCCACTTCTAGTTGCTGATTTCTTTCATATAAGAAATTTTGA 4585
Db 1141 CATCATTTCCAAATCTATCCACTTCTAGTTGCTGATTTCTTTCATATAAGAAATTTTGA 1200
Qy 4586 GATGTACGAAAAAATGTGACACCTTAAATCCATGGGATAGGCTTTTCAGTACTGTTAT 4645
Db 1201 GATGTACGAAAAAATGTGACACCTTAAATCCATGGGATAGGCTTTTCAGTACTGTTAT 1260
Qy 4646 ATCGCTTACCTGAGTGTACTGTGGATTTTTCCTCTTACAATCTATGAGAAAAAATA 4705
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Qy 4706 TGAGGAGCATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAGCTTAAAAA 4765
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 18:55:21 ; Search time 8094 Seconds
(without alignments)
19593.119 Million cell updates/sec

Title: US-10-005-338B-1

Perfect score: 6525

Sequence: 1 aaatgtgatattttctct.....ttgatcataataagtgaaat 6525

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	2934.4	45.0	3950 11	AK047188
2	2807	43.0	3831 11	AK046203
3	1209.6	18.5	1529 11	AK034961
4	1182	18.1	1346 11	U66672

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

AK047188

LOCUS

DEFINITION

AK047188

Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length

enriched library, clone:B930033A02 product:ATP-BINDING CASSETTE

PROTEIN homolog [Homo sapiens], full insert sequence.

AK047188

VERSION

AK047188.1

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1

Carninci, P. and Hayashizaki, Y.

AUTHORS

TITLE

High-efficiency full-length cDNA cloning

JOURNAL

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

99279253

PUBMED

10349636

REFERENCE

2

5	837	12.8	850	14	CD250953	CD250953 AGENCOURT
6	761.4	11.7	872	13	BC022933	BC022933 AGENCOURT
7	760.6	11.7	809	11	BC029426	BC029426 Homo sapi
8	741.4	11.4	773	13	BQ441353	BQ441353 AGENCOURT
9	731	11.2	747	13	BU686259	BU686259 UI-CF-DUI
10	722.4	11.1	771	10	BG564439	BG564439 602584385
11	719.4	11.0	793	14	CB241963	CB241963 UI-CF-FNO
12	681.6	10.4	756	10	BG435656	BG435656 602506942
13	680.4	10.4	744	9	AL700140	AL700140 DKFPZp686H
14	676.4	10.4	697	13	BO774317	BO774317 UI-H-EZ1-
15	668	10.2	926	13	BU146839	BU146839 AGENCOURT
16	661.6	10.1	728	13	BU623566	BU623566 UI-H-FG1-
17	655.4	10.0	792	10	BG564921	BG564921 602589884
18	652.4	10.0	800	13	BU750944	BU750944 CH3#036.H
19	646	9.9	735	12	BG926885	BG926885 HNC24-1-E
20	641	9.8	664	14	CB044826	CB044826 NISC gc06
21	634.4	9.7	670	10	BG570726	BG570726 602591840
22	633	9.7	633	14	CA773136	CA773136 im60B03.y
23	631.8	9.7	3890	11	BC053340	BC053340 Mus muscu
24	630.4	9.7	768	13	BU853701	BU853701 AGENCOURT
25	628.6	9.6	724	14	CB962917	CB962917 AGENCOURT
26	625.2	9.6	694	10	BF969534	BF969534 602271862
27	623	9.5	623	14	CA773849	CA773849 im58404.y
28	617	9.5	642	14	CA773183	CA773183 im60G04.y
29	612.4	9.4	614	14	CA771132	CA771132 io71b12.x
30	610.8	9.4	3357	11	BC037309	BC037309 Homo sapi
31	610.2	9.4	4119	11	AK029256	AK029256 Mus muscu
32	589.6	9.0	898	10	BG192651	BG192651 RST11768
33	586.8	9.0	961	14	CD242338	CD242338 AGENCOURT
34	583.8	8.9	589	10	BG149983	BG149983 nad50a05.
35	583.6	8.9	678	10	BE220217	BE220217 hv69f11.x
36	573.6	8.8	581	14	CA941420	CA941420 ir34h12.x
37	573.2	8.8	578	13	BU069128	BU069128 im58404.x
38	572.4	8.8	629	14	CA771439	CA771439 io71b12.y
39	565.8	8.7	608	9	AW131017	AW131017 xe68f06.x
40	561.6	8.6	570	2	HS0090776	Bx497427 Homo sapi
41	561.2	8.6	622	13	BU952395	BU952395 io74a05.x
42	559.4	8.6	769	14	CD349566	CD349566 UI-M-FY0-
43	557.6	8.5	3300	11	AK085555	AK085555 Mus muscu
44	553.2	8.5	571	14	W63628	W63628 zc56f10.r1
45	547.6	8.4	639	12	BG928068	BG928068 HNC16-1-A

Db 541 AACTGGTAGCCGCAAGTCCTTTCTAAGTCCAGCAACCTTCGTAGGTGTGGTTTTCTCAAGACA 600
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Db 601 CCATGTCCTATGAACCTTCGTTTTTTTCCCTGAAATGATTCAGTGTCTTCTATTTATATGA 660
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Qy 1531 CAGTTTTACAGCATCCATAGATGCTGCCATTATACAGTTGAAGCAACATGTTCTCTTT 1590
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Qy 1651 ATACCTTTCCCGAGGAGTAAATTTTAAATATACCTAGTTATAGCAATTTTCACTTTTGGAT 1710
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Db 1021 TTTTCTTATGCTCTTTATGGCTGTCATGCGCAACAGCTTCTGTTATTTCCCTCAGA 1080
Qy 1891 GTAGCAGCATGTGATATTTCTGCTTTTCTTTTATGATATATCATCTGATTTTGTG 1950
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Qy 1951 CTTTAAATGTCGACACCTCTTTTAAATAATCAAAACATGCGGAATAGTTGAATTTTTTG 2010
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Qy 2071 CGTTAGTGGCTTTTCAGTCTCTTCTGTCACCTGCTACTTTTGTGATTTGATTTGACAGG 2130
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Qy 2251 CTGTCTATCTTGATCAAGTCATTTCCAGGGAAATTTGGCTTTACCGAGATCATCTTTATTT 2310
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Qy 2311 TTCTGAGCCCTTCATATGCTCAAGAGTAAAGAAATATGAGGAGTTATCGAGGGCA 2370
Db 1501 TTTTGAAGCCCATCGTATTTGCTCAAAACAAAGAAACTATAAGGAGCTATCGAGGGCA 1560
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Qy 2671 CAAGAAAAATGATTTGGCATTTTGTCCAAGTTAGATATACACTTTTGTGTTTGTGACAGTAG 2730
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Qy 2731 AGAAAAATTTATCAATTTTGGCTTCAATCAAGGGATACACAGCAACATATATAACAAG 2790
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Qy 2791 AAGTGCAGAGGTTTTTACTAGATTTTATAGACATGACAGACTATCAAGAGATAACCAAGCTAAAA 2850
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Qy 2851 AATTAAAGTGGTGTCAAAAAAGAAAGCTGTCTATTAGGAATTTGCTTTTGGGAACCCAA 2910
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Qy 2911 AGATACCTGCTGCTAGACAGGCTTACAGCAGGAATGAGCCCTCTCTCGCATATTTGTT 2970
Db 2101 AGATACCTGCTGCTAGACAGGCTTACAGCAGGAATGAGCCCTCTCTCGCATATTTGTT 2160
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Db 2161 GGAATCTTTTAAATAACAGAAAGCCAAATCGGGTGCAGTGTTCAGTACTCATTTCTATGG 2220
Qy 3031 ATGAAGCTGACATCTTTGCGAGATAGAAAGCTGTGATATCAAGAGAAATGCTCAAAATGTG 3090
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Qy 3271 ACAATTTTTCAGTGTGTTTCTGCGCTTAGACAGTCAATTTTAAAGTTGGGTGTCAATTTCT 3330
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AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 3831)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tonaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
COMMENT	ENCODE library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers
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ORIGIN	
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Qy 5206 GAGCTGTCAAAGGAATCAGTGCAGTGCATGAAGAAAGTCATAAGTCGAATACACATG 5265
Db 421 GAGCTGTCAAAGGAATCAGTGCAGTGCATGAAGAAAGTCATAAGTCGAATACACATG 480
Qy 5266 CACTTGATTTAAAGAACATCTTCAGAAAGCTGTAAGAAACTACCTGAGGAATCAAC 5325
Db 481 CACTTGATTTAAAGAACATCTTCAGAAAGCTGTAAGAAACTACCTGAGGAATCAAC 540
Qy 5326 GAAAGTGTGTTTGTCTAAGTATGCTAGGGAATCTCAGATTACTTTCTAGATGAAC 5385
Db 541 CGAAAGTGTGTTTGTCTAAGTATGCTAGGGAATCTCAGATTACTTTCTAGATGAAC 600
Qy 5386 CATCTACAGTATGGATCCCAAA--GCCAAACAGCACATGTGGCGAGCAATTCGAATGC 5443
Db 601 CATCTACAGTATGGATCCCAAAATGCCAAACATGCACATGTGCATCAATTCGAATGC 660
Qy 5444 ATTTAAACAGAAAGCGGCTGTATTCTGACCACTCATCTATATGAGAGGAGGAGGC 5503
Db 661 AT-----NNAAGCGGGCTGTATTCTGACCCTCACTATATGAGGAGGAGGAGGC 711
Qy 5504 TGCTGTGATCGAGTACATCATGTGTCTGGGAGTAAAGTATTCGGAACAGTACA 5563
Db 712 TGCTGTGATCGAGTACATCATGTGTCTGGGAGTAAAGTATTCGGAACAGTACA 771
Qy 5564 ACATCTAAAGAGTAAATTTGGAAAGGCTACTTTTGGAAATTAATTTGAA--GGAATGGA 5622
Db 772 ACATCTAAAGAGTAAATTTGGAAAG--NACTTTTGGAAATTAATTTGAA--GGAATGGA 829
Qy 5623 TAGAAACCTTAGAAG--TAGACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCA 5681
Db 830 TAGAAACCTTAGAAGCTAGACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCA 889
Qy 5682 AGCGTGCAGAAAGCTTTTCTTATTTTGCCTATATAATCTCTAGGAGAGATGTTTTCAG 5741
Db 890 AGCGTGCAGAAAGCTTTTCTTATTTTGCCTATATAATCTCTAGGAGAGATGTTTTCAG 948
Qy 5742 TCCCTTTTCAAACTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGGCAATTTGAAGAA 5801
Db 949 TCCCTTTTCAAACTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGGCAATTTGAAGAA 1007
Qy 5802 TATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGACTCCTAAAGAACAGAG 5861
Db 1008 TATAGC--TTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGACTCCTAAAGAACAGAG 1066
Qy 5862 GAGGAGATATAGTGTGGAACCTTTTAAAGCAGACACTTTTGGTGGGACCAACACAGAA 5921
Db 1067 GAGGAGATATAGTGTGGAACCTTTTAAAGCAGACACTTTTGGT--GGAAACCAACAGAA 1125
Qy 5922 GATAGAGTAGTATTTTGAATTTTGTATTGTTTCGGTCTGCTTACTGGGACTTTCTTTCTTTT 5981
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Db 1126 GATAGAGTAGTATTTTGAATTTTGTATTGTTGGTCTGCTTACTGGGACTTTCTTTCTTTT 1185
Qy 5982 CACTTAATTTTAACTTTTGGTTTAAAGATTTTATTTGGAATGTAAGTGAACCAAG 6041
Db 1186 CACTTAATTTTAACTTTTGGTTTAAAGATTTTATTTGGAATGTAAGTGAACCAAG 1245
Qy 6042 AACGCACCTTGAATTTTCTTAAGCTCCTTAATTAATTAAGTGAA 6101
Db 1246 AACGCACCTTGAATTTTCTTAAGCTCCTTAATTAATTAAGTGAA 1305
Qy 6102 TTCTTTAAATAAAACGTATGATTAATTAAGTGAA 6135
Db 1306 TTCTTTAAATAAAACGTATGATTAATTAAGTGAA 1339

RESULT 5
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LOCUS AGENCOURT 14214041 NIH MGC 179 Homo sapiens cDNA clone
DEFINITION IMAGE:30385589 5', mRNA sequence.
ACCESSION CD250953
VERSION CD250953.1 GI:31011419
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 850)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM452 row: o column: 06
High quality sequence stop: 719.
Location/Qualifiers
source
1..850
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30385589"
/tissue_type="Pituitary"
/lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
/notes="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV
(destroyed); Site 2: NotI; Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon cloning
). Average insert size 1.1 kb. Library was constructed by
(invitrogen). Note: this is a NIH MGC Library."
BASE COUNT 284 a 143 c 183 g 238 t 2 others
ORIGIN
|||||
Query Match 12.8%; Score 837; DB 14; Length 850;
Best Local Similarity 99.8%; Pred. No. 3.7e-113;
Matches 848; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 5014 ATGGTCTGCGCAAAAGCACAAATTTATTAAATA-TTCTGTTGGTGATATTGAACCAACTTCA 5072
Db 1 ATGGTCTGCGCAAAAGCACAAATTTATTAAATTTCTGTTGGTGATATTGAACCAACTTCA 60
Qy 5073 GGCCAGGTATTTTAGGAGATTTCTTTCAGAGACAAGTGAAGATGATGATTCACCTGAAG 5132
Db 1125
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Db 61 GGCAGGATATTTTAGGAGATTAATCTTTCAGACAAGTGAAGATGATGATTCACCTGAAG 120
Qy 5133 TGATGGTTACTGTCTCAGATAAACCCTTTTGTGCCGATACACTACATTGTCAGGAACAT 5192
Db 121 TGTATGGGTTACTGTCTCAGATAAACCCTTTTGTGCCGATACACTACATTGTCAGGAACAT 180
Qy 5193 TTTGAAATTTATGAGCTGTCAAAGGAATGAGTGCAGTGACATGAAAGAAAGTCATAAGT 5252
Db 181 TTTGAAATTTATGAGCTGTCAAAGGAATGAGTGCAGTGACATGAAAGAAAGTCATAAGT 240
Qy 5253 CGAATAACACATGACCTTGAATTTAAAGAAACATCTTCAGAAAGACTGTAAAGAAACCTACCT 5312
Db 241 CGAATAACACATGACCTTGAATTTAAAGAAACATCTTCAGAAAGACTGTAAAGAAACCTACCT 300
Qy 5313 GCAGGAATCAAAAGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACT 5372
Db 301 GCAGGAATCAAAAGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACT 360
Qy 5373 TTGCTAGATCAACATCTACAGGTATGATCCCAAGCCCAAGCAAGCAACATGTCGGCAGCA 5432
Db 361 TTGCTAGATCAACATCTACAGGTATGATCCCAAGCCCAAGCAAGCAACATGTCGGCAGCA 420
Qy 5433 ATTGCAACTGCAATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAG 5492
Db 421 ATTGCAACTGCAATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAG 480
Qy 5493 GAGCAGAGGCTGTGTGATCGATGCTATCATGTGTCTGGCAGTTAGATGATATC 5552
Db 481 GAGCAGAGGCTGTGTGATCGATGCTATCATGTGTCTGGCAGTTAGATGATATC 540
Qy 5553 GGAACAGTACACATCTAAAGAGTAAATTTGAAAAAGGCTACTTTTGGAAATTAATTTG 5612
Db 541 GGAACAGTACACATCTAAAGAGTAAATTTGAAAAAGGCTACTTTTGGAAATTAATTTG 600
Qy 5613 AAGGACTGGATAGAAAACCTTAGAAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTC 5672
Db 601 AAGGACTGGATAGAAAACCTTAGAAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTC 660
Qy 5673 CAAAATCAAGCGCTGAGGAAGTTTCTTCTATTTTGGCTTATAAATTCCTAGGAA 5732
Db 661 CAAAATCAAGCGCTGAGGAAGTTTCTTCTATTTTGGCTTATAAATTCCTAGGAA 720
Qy 5733 GATGTTCAAGTCCCTTTCACAACTCTTTTAAAGCTGGAAGCAAGCAATGCTTTTGGC 5792
Db 721 GATGTTCAAGTCCCTTTCACAACTCTTTTAAAGCTGGAAGCAAGCAATGCTTTTGGC 780
Qy 5793 ATTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAA 5852
Db 781 ATTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAA 840
Qy 5853 GAACAAGAGG 5862
Db 841 GAACAAGAGG 850

RESULT 6
BQ722933
LOCUS
DEFINITION
AGENCY 8100461 Lupski sympathetic_trunk Homo sapiens cdna clone
IMAGE:6190464 5', mRNA sequence.
ACCESSION
BQ722933
VERSION
BQ722933.1 GI:21861819
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 872)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
```

Tissue Procurement: Dr. James R. Lupski
cdna Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13589 row: f column: 01
High quality sequence stop: 717.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6190464"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski sympathetic trunk"
/note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
Not1; site_2: SalI; cdna made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

BASE COUNT 285 a 149 c 193 g 245 t

ORIGIN

Query Match 11.7%; Score 761.4; DB 13; Length 872;

Best Local Similarity 97.9%; Pred. No. 4.6e-102; Indels 7; Gaps 5;

Matches 825; Conservative 0; Mismatches 11;

Qy 4970 TTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGTCCAAATGCTGTCGCAAAAG 5029

Db 1 TTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGTCCAAATGCTGTCGCAAAAG 60

Qy 5030 CACAATTAATTAATTTCTGTTGGTGATATTGAACCAACTTCAGCCAGGATTTTTAGG 5089

Db 61 CACAATTAATTAATTTCTGTTGGTGATATTGAACCAACTTCAGCCAGGATTTTTAGG 120

Qy 5090 AGATTATTTCTCAGAGACAAGTGAAGATGATTCACCTGAAGTGTATGGGTACTGTC 5149

Db 121 AGATTATTTCTCAGAGACAAGTGAAGATGATTCACCTGAAGTGTATGGGTACTGTC 180

Qy 5150 TCAGATAAAACCTTTGTGGCCAGATACCTACATTCAGGAAACATTTTGAAATTTATGGAGC 5209

Db 181 TCAGATAAAACCTTTGTGGCCAGATACCTACATTCAGGAAACATTTTGAAATTTATGGAGC 240

Qy 5210 TGTCAAAGGAATGAGTGCAGATGCAATGAAAGAGTCAATAAGTCAATTAACACATGCACT 5269

Db 241 TGTCAAAGGAATGAGTGCAGATGCAATGAAAGAGTCAATAAGTCAATTAACACATGCACT 300

Qy 5270 TGATTTAAAGAACATCTTCAGAGACCTGTAAGAACTACCTGCAGGAATCAAAAGAA 5329

Db 301 TGATTTAAAGAACATCTTCAGAGACCTGTAAGAACTACCTGCAGGAATCAAAAGAA 360

Qy 5330 GTTGTGTTTGTCTTAAGTATGCTAGGGAATCTCAGATTACTTTGCTAGATGAACCATC 5389

Db 361 GTTGTGTTTGTCTTAAGTATGCTAGGGAATCTCAGATTACTTTGCTAGATGAACCATC 420

Qy 5390 TACAGGTATGGATCCCAAGCCAAACAGCACATGTCGGCAGCAATTCGAATTCGAATTTAA 5449

Db 421 TACAGGTATGGATCCCAAGCCAAACAGCACATGTCGGCAGCAATTCGAATTCGAATTTAA 480

Qy 5450 AAACAGAAAGCGGCTGCTATTTCTGACCACTCATATATGAGGAGGAGGAGGCTGCTG 5509

Db 481 AAACAGAAAGCGGCTGCTATTTCTGACCACTCATATATGAGGAGGAGGAGGCTGCTG 540

JOURNAL
COMMENT

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: rgs@nih.gov
Tissue procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: AGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LCM2334 row: c column: 01
High quality sequence stop: 537.
Location/Qualifiers
1..773
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6101304"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NH MGC 82"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfII (ggccatcgcc); Site_2: SfII (ggccatcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
Alto, CA."

BASE COUNT 241 a 126 c 173 g 233 t
ORIGIN

Query Match 11.4%; Score 741.4; DB 13; Length 773;
Best Local Similarity 98.4%; Pred. No. 4.1e-99;
Matches 759; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 5323 AACGAAGTGTCTTGTCTTAAGTATGCTAGGATCTCTAGATCTCTAGATCTCTAGATG 5382
DB 3 AAGCAAGTGTGTCTTGTCTTAAGTATGCTAGGATCTCTAGATCTCTAGATCTCTAGATG 62
QY 5383 AACCATCTACAGGTATGATGCCAAAGCCAAAGCAGCAGCATGTGGCAGCAATTCGAATG 5442
DB 63 AACCATCTACAGGTATGATGCCAAAGCCAAAGCAGCAGCATGTGGCAGCAATTCGAATG 122
QY 5443 CATTTAAAAACAGAACCGGGCTGCTATTCTGACCACTACTATATGAGGAGGAGG 5502
DB 123 CATTTAAAAACAGAACCGGGCTGCTATTCTGACCACTACTATATGAGGAGGAGGAGG 182
QY 5503 CTGCTGTGATCGAGTATCATGTGTCCTGGCAGTTAAGATGATGCGAACAGTAC 5562
DB 183 CTGCTGTGATCGAGTATCATGTGTCCTGGCAGTTAAGATGATGCGAACAGTAC 242
QY 5563 AACATCTAAAGAGTAAATTTGGAAAGCGTACTTTTGGAAATTAATTAAGAGTACGGA 5622
DB 243 AACATCTAAAGAGTAAATTTGGAAAGCGTACTTTTGGAAATTAATTAAGAGTACGGA 302
QY 5623 TAGAAAACTTAGAGTACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCAA 5682
DB 303 TAGAAAACTTAGAGTACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCAA 362
QY 5683 GCCGTGAGGAAGTTTCTCTTCTATTTTGGCTTATATAAATTCCTAAGGAGATGTCAGT 5742
DB 363 GCCGTGAGGAAGTTTCTCTTCTATTTTGGCTTATATAAATTCCTAAGGAGATGTCAGT 422
QY 5743 CCCTTTCACAACTCTTTTAAAGCTGGAAGCAATCAATGCTTTTGGCAATTAAGAGAT 5802
DB 423 CCCTTTCACAACTCTTTTAAAGCTGGAAGCAATCAATGCTTTTGGCAATTAAGAGAT 482
QY 5803 ATAGCTTTCTCAGCAACATTTGGAACAGAGTTTGTGAGAACTCACTAAAGAACAGAGG 5862
DB 483 ATAGCTTTCTCAGCAACATTTGGAACAGAGTTTGTGAGAACTCACTAAAGAACAGAGG 542

QY 5863 AGGAAGATAATAGTTGTGGAACTTTAAACAGCAGCAGCTTTGTGGAGAACAGCAAGAAG 5922
DB 543 AGGAAGATAATAGTTGTGGAACTTTAAACAGCAGCAGCTTTGTGGAGAACAGCAAGAAG 602
QY 5923 ATAGAGTAGTATTTGAATTTGATTTGTTTGGTCTGCTTACTGGGACTTCTTTCTTTTC 5982
DB 603 ATAGAGTAGTATTTGAATTTGATTTGTTTGGTCTGCTTACTGGGACTTCTTTCTTTTC 662
QY 5983 ACTTAATTTTAACTTTGTTTAAAGAGTTTATTTGGAATGTAAGTGGAGAACCAAGA 6042
DB 663 ACTTAATTTTAACTTTGTTTAAAGAGTTTATTTGGAATGTAAGTGGAGAACCAAGA 721
QY 6043 ACGCAGTTGAAATTTTCTAAGCTCTTAAATGAAATGCTGTGTTGTG 6093
DB 722 ACGCAGTTGAAATTTTCTAAGCTCTTAAATGAAATGCTGTGTTGTG 772

RESULT 9
BU686259/c

LOCUS 747 bp mRNA linear EST 07-OCT-2002
DEFINITION UI-CF-DUI-adn-m-03-0-UI.s1 UI-CF-DUI Homo sapiens cDNA clone
UI-CF-DUI-adn-m-03-0-UI 3', mRNA sequence.

ACCESSION BU686259
VERSION BU686259.1 GI:23540987
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 747)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

Location/Qualifiers
1..747
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/db_xref="taxon:9606"
/clone="UI-CF-DUI-adn-m-03-0-UI"
/tissue_type="Primary Lung Epithelial Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-DUI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-DUI is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains

a library tag sequence that is located between the Not I site and the (d)18 tail. The sequence tag for this library is GCGTGTAGGC.

TAG LIB=UI-CF-DUI

TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368

TAG_SEQ=GCGTGTAGGC

BASE COUNT 230 a 153 c 112 g 252 t

ORIGIN

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Query Match 11.2%; Score 731; DB 13; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.4e-97;
Matches 731; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5405 CAAAGCCAAACAGCACATGTGGCGAGCAATTCGAATTCGATTTTAAACACAGAAAGCGGC 5464
Db 747 CAAAGCCAAACAGCACATGTGGCGAGCAATTCGAATTCGATTTTAAACACAGAAAGCGGC 688
QY 5465 TGCTATTCGACCACTCAGTATATGAGGAGCGGAGCGCTGTCTGTGATCGATAGCTAT 5524
Db 687 TGCTATTCGACCACTCAGTATATGAGGAGCGGAGCGCTGTCTGTGATCGATAGCTAT 628
QY 5525 CATGTGCTCTGGCAGTTAAGATGTATCGGAACAGTACACATCTAAAGAGTAAATTGG 5584
Db 627 CATGTGCTCTGGCAGTTAAGATGTATCGGAACAGTACACATCTAAAGAGTAAATTGG 568
QY 5585 AAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGATAGAAACCTAGAACTAGACCG 5644
Db 567 AAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGATAGAAACCTAGAACTAGACCG 508
QY 5645 CTTTCAAAGAAATTCAGTATATTTTCCAAATGCAAGCGCTCAGGAAAGTTTCTTC 5704
Db 507 CTTTCAAAGAAATTCAGTATATTTTCCAAATGCAAGCGCTCAGGAAAGTTTCTTC 448
QY 5705 TATTTGGCTTATAAATTCCTAAGGAGATGTTTCAGTCCCTTCACAATCTTTTAA 5764
Db 447 TATTTGGCTTATAAATTCCTAAGGAGATGTTTCAGTCCCTTCACAATCTTTTAA 388
QY 5765 GCTGGAAGAGCTAAACATGCTTTTGCAATTTGAAGATATAGCTTTTCTCAAGCAACAT 5824
Db 387 GCTGGAAGAGCTAAACATGCTTTTGCAATTTGAAGATATAGCTTTTCTCAAGCAACAT 328
QY 5825 GGAACAGGTTTTGTAGAACTCACTAAAGAACAGAGGAGGAGATATAGTTGTGAAC 5884
Db 327 GGAACAGGTTTTGTAGAACTCACTAAAGAACAGAGGAGGAGATATAGTTGTGAAC 268
QY 5885 TTTAAACAGCACATTTTGGTGGGACGAAACACAGAGATAGATATTTGAATTG 5944
Db 267 TTTAAACAGCACATTTTGGTGGGACGAAACACAGAGATAGATATTTGAATTG 208
QY 5945 TATTTGCTGCTGCTTACTTGGGACTTCTTTCTTTTCACTTAATTTTAACTTTGGTTA 6004
Db 207 TATTTGCTGCTGCTTACTTGGGACTTCTTTCTTTTCACTTAATTTTAACTTTGGTTA 148
QY 6005 AAAAGTTTTTTTATTTGAATGGTAACTCGAGAACCAAGACGCACTTGAATTTTCTAAG 6064
Db 147 AAAAGTTTTTTTATTTGAATGGTAACTCGAGAACCAAGACGCACTTGAATTTTCTAAG 88
QY 6065 CTCCTTAATTTGAATGCTGTTGTGTTGTTGTTGTTTCTTTTAAATAAAGATGAT 6124
Db 87 CTCCTTAATTTGAATGCTGTTGTGTTGTTGTTGTTTCTTTTAAATAAAGATGAT 28
QY 6125 AATTAAGTGAA 6135
Db 27 AATTAAGTGAA 17
```

RESULT 10

BG564439

LOCUS

DEFINITION 602584385F1 NIH_MGC_76 Homo sapiens cdna clone IMAGE:4712157 5',

ACCESSION BG564439

VERSION BG564439.1 GI:13572091

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST.

Homo sapiens (human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 771)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI553 row: i column: 22

High quality sequence stop: 763.

Location/Qualifiers

1. .771

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_76"

/notes="Organ: liver; Vector: pDNR-LIB (Clontech); Site: 1:

SfiI (ggcgctcgcc); Site 2: SfiI (ggcgctcgcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.85

Kb (range 1.0-4.0 Kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH MGC Library."

BASE COUNT 275 a 130 c 167 g 199 t

ORIGIN

Query Match

Best Local Similarity 99.4%; Pred. No. 2.5e-96;

Matches 767; Conservative 0; Mismatches 1; Indels 4; Gaps 4;

QY 4721 AAGAAAAGATCCCTTTTTCAGAAACCTTTCAGAAAGTCTTAAAGTAGGAGCTTCAGA 4780

Db 1 AAGAAAAGATCCCTTTTTCAGAAACCTTTCAGAAAGTCTTAAAGTAGGAGCTTCAGA 60

QY 4781 ACCACCAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGA 4840

Db 61 ACCACCAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGA 120

QY 4841 GCTGATGGGTGTCAGTGTGTGAGGAGAAACCATCATTTATGCTCAGCAATTTGCATAA 4900

Db 121 GCTGATGGGTGTCAGTGTGTGAGGAGAAACCATCATTTATGCTCAGCAATTTGCATAA 180

QY 4901 AGAATATGATGACAAGAAAGATTTTCTTCTTCAAGAAAAGTAAAGAAAGTGGCACTAA 4960

Db 181 AGAATATGATGACAAGAAAGATTTTCTTCTTCAAGAAAAGTAAAGAAAGTGGCACTAA 240

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QY 5021 TGGCAAAAGCACAAATTTAATATTTCTGGTGTGATATTGAACCAACTTCAGGCCAGGT 5080

Db 301 TGGCAAAAGCACAAATTTAATATTTCTGGTGTGATATTGAACCAACTTCAGGCCAGGT 360

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Db 361 ATTTTATGAGGATATTCTTTTCAGAGACAAGTGAAGATGATGATTTCTGTAAGTGTATGGG 420


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VERSION      BG435656.1  GI:13342162
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1. (bases 1 to 756)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-f@mail.nih.gov
             Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LNL at:
             http://image.llnl.gov
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             adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor
             sequence: 5'-ATTCGAGGCGGCGGCCGACATG-dT(30)BN-3'
             (where B = A, C, or G and N = A, C, G, or T). Average
             insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
             contained inserts by PCR. This library was enriched for
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BASE COUNT   269 a 123 c 168 g 196 t
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Best Local Similarity 97.1%; Pred. No. 2.5e-90;
Matches 726; Conservative 0; Mismatches 19; Indels 3; Gaps 3;

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LOCUS DKF2686H03117_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKF2686H03117_5', mRNA sequence.
ACCESSION AL700140
VERSION AL700140.1 GI:19620673
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, H.W., Weil, B. and
Wiemann, S.
TITLE (S.)
JOURNAL Unpublished
COMMENT Contact: Ottenwaelder B
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MedGenomix (Martinsried/Germany) within the CDNA
sequencing consortium of the German Genome Project. No s1 sequence
available.
This clone (DKF2686H03117) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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LOCUS			
DEFINITION			
UI-H-EZ1-bca-d-17-0-UI.s1 NCI CGAP Ch2 Homo sapiens cDNA clone			
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BQ774317			
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VERSION			
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1 (bases 1 to 697)			
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
AUTHORS			
TITLE			
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
Tumor Gene Index			
JOURNAL			
Unpublished			
COMMENT			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs-remail.nih.gov			
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of			
Orthopaedics			
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa			
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa			
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa			
Clone Distribution: Clone distribution information can be obtained			
from Dr. M. Bento Soares, bento-soares@uiowa.edu			
The following repetitive elements were found in this cDNA			
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POLYA=Yes.			
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was constructed according to Bonaldo, Lennon and Soares,			
Genome Research, 6:791-806, 1996. First strand cDNA			
synthesis was primed with an oligo-dT primer containing a			
Not I site. Double stranded cDNA was ligated to an Ecor I			
adaptor, digested with Not I, and cloned directionally			
into pT73-Pac vector. The oligonucleotide used to prime			
the synthesis of first-strand cDNA contains a library tag			
sequence that is located between the Not I site and the			
(dT)18 tail. The sequence tag for this library is			
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DEFINITION	AGENCOURT 7978475	Lupski_dorsal_root_ganglion Homo sapiens	EST 03-SEP-2002
ACCESSION	BUI46839	clone IMAGE:6185202 5', mRNA sequence.	
VERSION	BUI46839.1	GI:22660371	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-x@mail.nih.gov CDNA Library Preparation: Life Technologies, Inc. CDNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LHAM13575 row: j column: 19 High quality sequence stop: 657.		

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Job time : 8102 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 16:31:11 ; Search time 15238 Seconds
(without alignments)
17517.740 Million cell updates/sec

Title: US-10-005-338B-1

Perfect score: 6525

Sequence: 1 aaatgtgatattttctct.....ttgatcataataagtgaaat 6525

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	6524	100.0	6525	6	AX473847 Sequence
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3	6122.8	93.8	6369	6	AX32931 Sequence
4	5373.2	82.3	5475	6	AX537473 Sequence
5	5255.8	80.5	5463	6	AX537470 Sequence
6	5247.4	80.4	5262	6	AX417828 Sequence
7	5039	77.2	5096	9	HS275973 Homo sapi
8	4918.4	75.4	4929	6	AX417824 Sequence
9	4807.4	73.7	4917	6	AX537472 Sequence
10	4754.8	72.9	4785	6	AX417826 Sequence
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12	3877	59.4	5170	10	RNO426052 Rattus no
13	3868.8	59.3	4929	10	AB097675 Mus muscu
14	3816.2	58.5	4945	10	RNO550165 Rattus no
15	3258.2	49.9	3347	9	AK094416 Homo sapi
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18	2795.2	42.8	3112	9	AB067475 Homo sapi
19	2773.6	42.5	2845	9	HS275973 Homo sapi
20	1731.8	26.5	1943	9	AK096664 Homo sapi
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25	1182	18.1	1346	6	AX410760 Sequence
26	1150.4	17.6	6181	6	AX473850 Sequence
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ALIGNMENTS

RESULT 1	AX473847	AX473847	6525 bp	DNA	linear	PAT 09-AUG-2002
LOCUS	Sequence 1 from Patent WO0246458.					
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ACCESSION	AX473847					
VERSION	AX473847.1	GI:22208006				
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Denefle, P., Rosier-Montus, M.F., Prades, C., Arnould-Reguigne, I.,					
	Duverger, N., Allikmets, R. and Dean, M.					
TITLE	Nucleic acids of the human abca5, abca6, abca9, and abca10 genes,					

vectors containing such nucleic acids and uses thereof

JOURNAL Patent: WO 0246458-A 1 13-JUN-2002;
Aventis Pharma S.A. (FR); The Secretary, Department of Health and
Human Services (US)

FEATURES
source

Location/Qualifiers
1. 6525
/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 1973 a 1108 c 1258 g 2185 t 1 others

ORIGIN

Query Match 100.0%; Score 6524; DB 6; Length 6525;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 6525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AAATGTTGATATTTCTCTTAGCAGCTGTCTCAACGAGTTAGGTTCAAGTCAATAAGTTT	60
Db	1	AAATGTTGATATTTCTCTTAGCAGCTGTCTCAACGAGTTAGGTTCAAGTCAATAAGTTT	60
Qy	61	CTACCCACATCTTTGAACTGTAGTGTCTATTTAGTTTATTTTCAAAAACCTTTTGCAG	120
Db	61	CTACCCACATCTTTGAACTGTAGTGTCTATTTAGTTTATTTTCAAAAACCTTTTGCAG	120
Qy	121	TACCTTTTGGTCTGTCTGTGTGCTTGCAGTGAACAGCTGGAATTTGGAAGTGTG	180
Db	121	TACCTTTTGGTCTGTCTGTGTGCTTGCAGTGAACAGCTGGAATTTGGAAGTGTG	180
Qy	181	CTGTCTGTTAGTTTCTCAAGCTTTTGTCTACACTAATAGGATTTGATTTATGTATG	240
Db	181	CTGTCTGTTAGTTTCTCAAGCTTTTGTCTACACTAATAGGATTTGATTTATGTATG	240
Qy	241	TCAGCTTGGGAATTTATCAGAAATTAATAAACAATTTTGTAGAGCTTTTCTGAGCTC	300
Db	241	TCAGCTTGGGAATTTATCAGAAATTTAATAAACAATTTTGTAGAGCTTTTCTGAGCTC	300
Qy	301	CTTTTCTATTTTGTCCCTCTTCTACTTTTGTCTTCCCTGCTGCTGCTTTCTATCCTCC	360
Db	301	CTTTTCTATTTTGTCCCTCTTCTACTTTTGTCTTCCCTGCTGCTGCTTTCTATCCTCC	360
Qy	361	AGCCAGAGCTAGTGTATTTCTCAATTTGTGTGTACACATTTGTGCAAGTGTCAACACC	420
Db	361	AGCCAGAGCTAGTGTATTTCTCAATTTGTGTGTACACATTTGTGCAAGTGTCAACACC	420
Qy	421	CATATCCAGGCCCCAATGTAGAGTGTAGAGAGAAAGCAAGGATTTGGCTCATCC	480
Db	421	CATATCCAGGCCCCAATGTAGAGTGTAGAGAGAAAGCAAGGATTTGGCTCATCC	480
Qy	481	TCCTTCAACAGATAGTTCATTTGAATAGAGAGAAAGGTTTTCCTGCTCAGAGTGTGGCT	540
Db	481	TCCTTCAACAGATAGTTCATTTGAATAGAGAGAAAGGTTTTCCTGCTCAGAGTGTGGCT	540
Qy	541	GCACTAGGCTTTTGTACTGTAGTCTGGCCCTGTATACATTTGCAATTTGCAATTTGGGG	600
Db	541	GCACTAGGCTTTTGTACTGTAGTCTGGCCCTGTATACATTTGCAATTTGCAATTTGGGG	600
Qy	601	ATACAGAGAAATTCAGAAAGAAAGATTTGCTATTTCTACATTTCCCTGAGCATTT	660
Db	601	ATACAGAGAAATTCAGAAAGAAAGATTTGCTATTTCTACATTTCCCTGAGCATTT	660
Qy	661	AAGACCTCCCTGCCCCATCTCAATTTCAAGCTTAAGGCTTTCTTGGAGCTGCCCTCTGT	720
Db	661	AAGACCTCCCTGCCCCATCTCAATTTCAAGCTTAAGGCTTTCTTGGAGCTGCCCTCTGT	720
Qy	721	GGGCGGTTGGGAGATACCAAGAGAGAAAGTCACTGTTGATATGGTGTATTTTCAA	780
Db	721	GGGCGGTTGGGAGATACCAAGAGAGAAAGTCACTGTTGATATGGTGTATTTTCAA	780
Qy	781	ATTCTGTCTACCTATTTTCAATGCTTCTTTTACTTTTTCAGAGCTGTGATTTGCTGCT	840
Db	781	ATTCTGTCTACCTATTTTCAATGCTTCTTTTACTTTTTCAGAGCTGTGATTTGCTGCT	840
Qy	841	CCATGCATTTCTGCTCCAGTTTCTTAAGAGAGACAGCTTGGAGTATGCTTAATCCATCTTAC	900

Db	841	CCATGCATTTCTGCTCCAGTTTCTTAAGAGAGACAGCTTGGAGTATGCTTAATCCATCTTAC	900
Qy	901	CTGGAGCTGAACAGCTGCTTTATTTTGCCTTAAATAATCATACAGTTTACTGCTGCGC	960
Db	901	CTGGAGCTGAACAGCTGCTTTATTTTGCCTTAAATAATCATACAGTTTACTGCTGCGC	960
Qy	961	TCCGGTTTGTGTTGTTGTTTCTCTTTAATAGGTTTATTCAGAAAAACATGTCACCTG	1020
Db	961	TCCGGTTTGTGTTGTTGTTTCTCTTTAATAGGTTTATTCAGAAAAACATGTCACCTG	1020
Qy	1021	CAATPAGGAGGTAGGAGTTTGGAGACAGACAGAAACCTTCTACTGAAGAAATTAATCTAA	1080
Db	1021	CAATPAGGAGGTAGGAGTTTGGAGACAGACAGAAACCTTCTACTGAAGAAATTAATCTAA	1080
Qy	1081	TTAATGACAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCCATATTTTATTTAT	1140
Db	1081	TTAATGACAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCCATATTTTATTTAT	1140
Qy	1141	TTTGGTTAATTAATTAAGCATGATGCATCAAAATAAGAAATATGAAGAGTGCCTAATA	1200
Db	1141	TTTGGTTAATTAATTAAGCATGATGCATCAAAATAAGAAATATGAAGAGTGCCTAATA	1200
Qy	1201	TAGAACTCAATCTATGACCAAGTTTACTCTTTCTAATCTAATCTTGGATATATCTCAG	1260
Db	1201	TAGAACTCAATCTATGACCAAGTTTACTCTTTCTAATCTAATCTTGGATATATCTCAG	1260
Qy	1261	TGACTAATTAATTAAGAGCATCATGCAAGAAAGTGTCTACTGATCATCTACTGATGCA	1320
Db	1261	TGACTAATTAATTAAGAGCATCATGCAAGAAAGTGTCTACTGATCATCTACTGATGCA	1320
Qy	1321	TAAATPACTGAAGATATACAAATGAAGAAAGAAATGTTAAACATCAAGTCTCTTAAGCCG	1380
Db	1321	TAAATPACTGAAGATATACAAATGAAGAAAGAAATGTTAAACATCAAGTCTCTTAAGCCG	1380
Qy	1381	GCAACTTTGTAGGTGTGGTTTCAAGACTCCATGTCTATGAACTCGTTTCTTCTGCTG	1440
Db	1381	GCAACTTTGTAGGTGTGGTTTCAAGACTCCATGTCTATGAACTCGTTTCTTCTGCTG	1440
Qy	1441	ATATGATTTCCAGTATCTTCTATTTATGAAATCAAGAGCTGGCTGTTCAAAATCATG	1500
Db	1441	ATATGATTTCCAGTATCTTCTATTTATGAAATCAAGAGCTGGCTGTTCAAAATCATG	1500
Qy	1501	AGGCTGCTCAGTACTGCTCCTCAGTTTCAAGCTTTTCAAGAGCTGAGTCACTAAGCTG	1560
Db	1501	AGGCTGCTCAGTACTGCTCCTCAGTTTCAAGCTTTTCAAGAGCTGAGTCACTAAGCTG	1560
Qy	1561	TTATACAGTTGAAGACCAATGTTCTTCTTGGAGGAGCTGGAGTCACTAAGCTGTTA	1620
Db	1561	TTATACAGTTGAAGACCAATGTTCTTCTTGGAGGAGCTGGAGTCACTAAGCTGTTA	1620
Qy	1621	TTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTAAATTTAATAT	1680
Db	1621	TTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTAAATTTAATAT	1680
Qy	1681	ACCTAGTTATAGCATTTTCACTTTTGGATATCTTTTGGCAATTCATATCGTAGCAGAAA	1740
Db	1681	ACCTAGTTATAGCATTTTCACTTTTGGATATCTTTTGGCAATTCATATCGTAGCAGAAA	1740
Qy	1741	AAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTTCATGATATGCTCTTTTGGC	1800
Db	1741	AAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTTCATGATATGCTCTTTTGGC	1800
Qy	1801	TTTCTGCGGTTCTCTATATACAGTTTAAATTTTCTTCTTCTTCTTCTTCTTCTTCTT	1860
Db	1801	TTTCTGCGGTTCTCTATATACAGTTTAAATTTTCTTCTTCTTCTTCTTCTTCTTCTT	1860
Qy	1861	TTGCGACAGCTTCTTTGTTTATTTCTCAAGTAGCAGCATTTGTGATATTTCTGCTTTT	1920
Db	1861	TTGCGACAGCTTCTTTGTTTATTTCTCAAGTAGCAGCATTTGTGATATTTCTGCTTTT	1920
Qy	1921	TCCTTTATGGATTAATCATCTGTAATTTTGTCTTAAATGCTGACCTCTTTTAAAAAT	1980
Db	1921	TCCTTTATGGATTAATCATCTGTAATTTTGTCTTAAATGCTGACCTCTTTTAAAAAT	1980

Db 1921 TCCTTTATGGATTATCACTGTATTTTTTTCGTTCTTAATGCTGACACCTCTTTTTAAAAAAT 1980
QY 1981 CAAAACATGTGGGAATAGTTGAATTTTTTGTGTACTGTGGCTTTTGGATTTATTTGGCCTTA 2040
Db 1981 CAAAACATGTGGGAATAGTTGAATTTTTTGTGTACTGTGGCTTTTGGATTTATTTGGCCTTA 2040
QY 2041 TGATAATCCCTCATAGAAAGTTTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCCTTTCTGTC 2100
Db 2041 TGATAATCCCTCATAGAAAGTTTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCCTTTCTGTC 2100
QY 2101 ACTGTACTTTTGTGATTTGATTTGTCACAGCTCATGCTATTTTAGAGATTTTAAATGAGGTG 2160
Db 2101 ACTGTACTTTTGTGATTTGTCACAGCTCATGCTATTTTAGAGATTTTAAATGAGGTG 2160
QY 2161 CTTCAATTTTCAAAATTTGACTGCGAGGCCATATCCTCTAAATATTACAAATATCATGCTCA 2220
Db 2161 CTTCAATTTTCAAAATTTGACTGCGAGGCCATATCCTCTAAATATTACAAATATCATGCTCA 2220
QY 2221 CACTTAATAGTATATCTATGCTCTTGGCTGTCTATCTTGATCAAGTCAATTCAGGGG 2280
Db 2221 CACTTAATAGTATATCTATGCTCTTGGCTGTCTATCTTGATCAAGTCAATTCAGGGG 2280
QY 2281 AATTTGGCTTACCGAGATCATCTTATATTTTCTGAGCCCTTCATATTTGGTCAAGGTA 2340
Db 2281 AATTTGGCTTACCGAGATCATCTTATATTTTCTGAGCCCTTCATATTTGGTCAAGGTA 2340
QY 2341 AAAGAAATTAATGAGGATTCAGAGGCCAATGTTAATGGAATATTAGTTTGTAGTGAA 2400
Db 2341 AAAGAAATTAATGAGGATTCAGAGGCCAATGTTAATGGAATATTAGTTTGTAGTGAA 2400
QY 2401 TTATTTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAGGCCATAAGAAATTTAGTGTATTC 2460
Db 2401 TTATTTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAGGCCATAAGAAATTTAGTGTATTC 2460
QY 2461 AGAAGACATACAGAAAGAGGTGAAATGTTGAGGCTTTTGAGAAATTTGTCAATTTGACA 2520
Db 2461 AGAAGACATACAGAAAGAGGTGAAATGTTGAGGCTTTTGAGAAATTTGTCAATTTGACA 2520
QY 2521 TATATGAGGTCAGATTAATGCTTCTGCTGACAGTGAACAGAGGAAAGTACATTTGA 2580
Db 2521 TATATGAGGTCAGATTAATGCTTCTGCTGACAGTGAACAGAGGAAAGTACATTTGA 2580
QY 2581 TGAATATTTCTTTGTGGACTCTGCCACCTTCTGATGGTTTGCATCTATATATGACACA 2640
Db 2581 TGAATATTTCTTTGTGGACTCTGCCACCTTCTGATGGTTTGCATCTATATATGACACA 2640
QY 2641 GAGTCTCAGAAATAGATGAATGTTTGAAGCAGAAATAATGATTTGGCAATTTGTCACAGT 2700
Db 2641 GAGTCTCAGAAATAGATGAATGTTTGAAGCAGAAATAATGATTTGGCAATTTGTCACAGT 2700
QY 2701 TAGATATACACTTTTGTATGTTTGCAGTAGAAGAAATTTATCAATTTTGGCTTCAATCA 2760
Db 2701 TAGATATACACTTTTGTATGTTTGCAGTAGAAGAAATTTATCAATTTTGGCTTCAATCA 2760
QY 2761 AAGGGATACCAGCCAAACAATATATACAGAAGTGCAGAGGTTTACTAGATTTAGACA 2820
Db 2761 AAGGGATACCAGCCAAACAATATATACAGAAGTGCAGAGGTTTACTAGATTTAGACA 2820
QY 2821 TGCAGACTATCAAGATAACAGCTAAAAATTTAAGTGTGGTCAAAAAAGAAAGCTGT 2880
Db 2821 TGCAGACTATCAAGATAACAGCTAAAAATTTAAGTGTGGTCAAAAAAGAAAGCTGT 2880
QY 2881 CATTAGGAATGCTGTTCTTGGGAACCAAGACTGCTGCTAGATGAACCAACAGCTG 2940
Db 2881 CATTAGGAATGCTGTTCTTGGGAACCAAGACTGCTGCTAGATGAACCAACAGCTG 2940
QY 2941 GAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATAACAGAAAGCCAAATC 3000
Db 2941 GAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATAACAGAAAGCCAAATC 3000
QY 3001 GGGTGACAGTGTTCAGTACTCATTTTCATGATGAAGCTGACATTTTTCAGATAGGAAAG 3060
Db 3001 GGGTGACAGTGTTCAGTACTCATTTTCATGATGAAGCTGACATTTTTCAGATAGGAAAG 3060

QY 3061 CTGTGATATCACAAGGAATGCTGAATGTGTGGTTCTTCAATGTTCTCTCAAAAGTAAAT 3120
Db 3061 CTGTGATATCACAAGGAATGCTGAATGTGTGGTTCTTCAATGTTCTCTCAAAAGTAAAT 3120
QY 3121 GGGGGATCGGCTTACCGCCCTGAGCATGTACATAGACAAATATTGTGCCACAGAAATCTCTTT 3180
Db 3121 GGGGGATCGGCTTACCGCCCTGAGCATGTACATAGACAAATATTGTGCCACAGAAATCTCTTT 3180
QY 3181 CTTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATACCAAGAAATGACCAACAAC 3240
Db 3181 CTTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATACCAAGAAATGACCAACAAC 3240
QY 3241 TTGTGTATAGCTTGCCTTTTCAAGGACATGGAACAAATTTTTCAGGTTTGTCTTCTGCCCTAG 3300
Db 3241 TTGTGTATAGCTTGCCTTTTCAAGGACATGGAACAAATTTTTCAGGTTTGTCTTCTGCCCTAG 3300
QY 3301 ACAGTCATTTCAAAATTTGGGTGTCTTTCTTATGTTGTTTCCATGACGACTTTTGGAAAGACG 3360
Db 3301 ACAGTCATTTCAAAATTTGGGTGTCTTTCTTATGTTGTTTCCATGACGACTTTTGGAAAGACG 3360
QY 3361 TATTTTAAAGCTTAGAAGTTTGAAGCAGAAATTTGACCAAGCAGATTTATAGTGTATTTACTC 3420
Db 3361 TATTTTAAAGCTTAGAAGTTTGAAGCAGAAATTTGACCAAGCAGATTTATAGTGTATTTACTC 3420
QY 3421 AGCAGCCACTTGGAGGAAGAAATGGATTTCAAAATCTTTTGTATGAAATGGAAACAGAGCTTAC 3480
Db 3421 AGCAGCCACTTGGAGGAAGAAATGGATTTCAAAATCTTTTGTATGAAATGGAAACAGAGCTTAC 3480
QY 3481 TTATTTCTTCTGAAACCAAGGCTTCTAGTGAAGCAACATGAGCCCTTTTGGAAACACAGAG 3540
Db 3481 TTATTTCTTCTGAAACCAAGGCTTCTAGTGAAGCAACATGAGCCCTTTTGGAAACACAGAG 3540
QY 3541 TGTATACAAATAGCAAAAGTTTCAATTTTACCTTTGAAACGTAAGTAAATCAGTGAGAT 3600
Db 3541 TGTATACAAATAGCAAAAGTTTCAATTTTACCTTTGAAACGTAAGTAAATCAGTGAGAT 3600
QY 3601 CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTGTGTTTCATC 3660
Db 3601 CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTGTGTTTCATC 3660
QY 3661 ACTTTTTAAAAATGCTGTGGTTCCCATCAAACTGTTCCAGACTTATATTTTCTAAAAAC 3720
Db 3661 ACTTTTTAAAAATGCTGTGGTTCCCATCAAACTGTTCCAGACTTATATTTTCTAAAAAC 3720
QY 3721 CTGGAGACAAACCAATATAACAAACAAAGTCTGCTTCTTCAAAATTTCTGCTGACTCAG 3780
Db 3721 CTGGAGACAAACCAATATAACAAACAAAGTCTGCTTCTTCAAAATTTCTGCTGACTCAG 3780
QY 3781 ATATCAGTCAATCTTATTTAGCTTTTTCACAAAGCCAGAAACATAATGTTGACGATGATTAATG 3840
Db 3781 ATATCAGTCAATCTTATTTAGCTTTTTCACAAAGCCAGAAACATAATGTTGACGATGATTAATG 3840
QY 3841 ACAGTCACTATGATATCCGTTCCCTCCCACTAGTGGCTTTTAAATGATGATGATTCAGAAA 3900
Db 3841 ACAGTCACTATGATATCCGTTCCCTCCCACTAGTGGCTTTTAAATGATGATGATTCAGAAA 3900
QY 3901 AGGACTATGTTTTCAGCTGTTTTCACAGTACTATGTTTATTTTCTTACCTATATTTAG 3960
Db 3901 AGGACTATGTTTTCAGCTGTTTTCACAGTACTATGTTTATTTTCTTACCTATATTTAG 3960
QY 3961 TGAATATCAATTTAGTAACTACTTCTTTTATCATTTTAAATGTGACTGAAACCACATCT 4020
Db 3961 TGAATATCAATTTAGTAACTACTTCTTTTATCATTTTAAATGTGACTGAAACCACATCT 4020
QY 4021 GGAGTACCCCATTTCTTTCAAGAAATTTACTGATAGTTTTTAAAAATGAGCTGATTTTC 4080
Db 4021 GGAGTACCCCATTTCTTTCAAGAAATTTACTGATAGTTTTTAAAAATGAGCTGATTTTC 4080
QY 4081 AAGCAGCTTTGCTTGAATCATTTGTTACTGCAATGCACTTACTTTTGCATGCAAAATG 4140
Db 4081 AAGCAGCTTTGCTTGAATCATTTGTTACTGCAATGCACTTACTTTTGCATGCAAAATG 4140

Qy 4141 CAGAGATCAATAAGATCAAAAGCTTATATCACTAACTTTTTCAGGTCTTTTGGCCATCTG 4200
Db 4141 CAGAGATCAATAAGATCAAAAGCTTATATCACTAACTTTTTCAGGTCTTTTGGCCATCTG 4200
Qy 4201 CATATTGGATTGGACAAAGCTGTTGGATATCCCTTATTTTTTATCATCTTATTTTGA 4260
Db 4201 CATATTGGATTGGACAAAGCTGTTGGATATCCCTTATTTTTTATCATCTTATTTTGA 4260
Qy 4261 TGGCTAGGAAGCTTACTGGCAATTTTCAATGGATATATTTTTTATCATCTTATTTTGA 4320
Db 4261 TGGCTAGGAAGCTTACTGGCAATTTTCAATGGATATATTTTTTATCATCTTATTTTGA 4320
Qy 4321 CTGTGGTTTTTGGCTTATTTGGTTATGTTCCATCAGTTATTTCTGTTCACTTATTTGCTT 4380
Db 4321 CTGTGGTTTTTGGCTTATTTGGTTATGTTCCATCAGTTATTTCTGTTCACTTATTTGCTT 4380
Qy 4381 CTTTACCTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCATTTATCTATCTGTGG 4440
Db 4381 CTTTACCTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCATTTATCTATCTGTGG 4440
Qy 4441 CAGGTTGNCCTGTATGGCAATCACTGAATTAATCTTTTATGGGATACAAATTTGCAA 4500
Db 4441 CAGGTTGNCCTGTATGGCAATCACTGAATTAATCTTTTATGGGATACAAATTTGCAA 4500
Qy 4501 CTATTTCTTCAATATGCTTTTGTATCATCTCAATCTATCCATCTTAGGTTGCTCA 4560
Db 4501 CTATTTCTTCAATATGCTTTTGTATCATCTCAATCTATCCATCTTAGGTTGCTCA 4560
Qy 4561 TTTTCTTTTCAATAAGATTTTCTTGGAAAGATGTAGCAAAAATGTGACCACTATTAATCCAT 4620
Db 4561 TTTTCTTTTCAATAAGATTTTCTTGGAAAGATGTAGCAAAAATGTGACCACTATTAATCCAT 4620
Qy 4621 GGGATAGGCTTTTCAATAGCTTTTATATCGCTTCACTGCAAGTGTACTGTCGATTTTCC 4680
Db 4621 GGGATAGGCTTTTCAATAGCTTTTATATCGCTTCACTGCAAGTGTACTGTCGATTTTCC 4680
Qy 4681 TCTTACAATATCTATGAGAAAAATATGGAGGAGATCAATAAGAAAGATCCCTTTTCA 4740
Db 4681 TCTTACAATATCTATGAGAAAAATATGGAGGAGATCAATAAGAAAGATCCCTTTTCA 4740
Qy 4741 GAAACCTTTTCAAGAGCTTAAATAATAGGAAGCTTCCAGAACCAACAGACAATGAGGATG 4800
Db 4741 GAAACCTTTTCAAGAGCTTAAATAATAGGAAGCTTCCAGAACCAACAGACAATGAGGATG 4800
Qy 4801 AAGATGAAGTGTCAAGCTTAAAGATCAAGGCTTAAAGGCTTAAAGGCTTAAAGGCTT 4860
Db 4801 AAGATGAAGTGTCAAGCTTAAAGATCAAGGCTTAAAGGCTTAAAGGCTTAAAGGCTT 4860
Qy 4861 GTGAGGAGAAACCATCTCATTTATGTCAGCAATTTGCAATAAGAAATATGATGACAAGAAAG 4920
Db 4861 GTGAGGAGAAACCATCTCATTTATGTCAGCAATTTGCAATAAGAAATATGATGACAAGAAAG 4920
Qy 4921 ATTTTCTTTTCAAGAAAAATGAAAGAGTGGCAACTAAATACATCTCTTTCTGTGTGA 4980
Db 4921 ATTTTCTTTTCAAGAAAAATGAAAGAGTGGCAACTAAATACATCTCTTTCTGTGTGA 4980
Qy 4981 AAAAGAGAGATCTTAGGACTATTTGGTCCAAATGGTGTGCAAAAGCACAATTTATTA 5040
Db 4981 AAAAGAGAGATCTTAGGACTATTTGGTCCAAATGGTGTGCAAAAGCACAATTTATTA 5040
Qy 5041 ATATTCTGGTTGGTGATTTGAACCAACTTTGAGCCAGGTATTTTATGAGGATTTCTTT 5100
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Qy 5101 CAGAGACAAGTGAAGATGATTTCACTGAAGTGTATGGGTTACTGTCTCTCAGATAAAC 5160
Db 5101 CAGAGACAAGTGAAGATGATTTCACTGAAGTGTATGGGTTACTGTCTCTCAGATAAAC 5160
Qy 5161 CTTTGTGGCAGATCTACATTTGCAGAACTTTTGAATTTTATGGAGTGTCAAGAGAA 5220
Db 5161 CTTTGTGGCAGATCTACATTTGCAGAACTTTTGAATTTTATGGAGTGTCAAGAGAA 5220
Qy 5221 TGAGTGAAGTGAATGAAAGAGTCTAATAGTCGAATTAACATGCACTTTGATTTAAAG 5280

Db 5221 TGAGTGAAGTGAATGAAAGAGTCTAATAGTCGAATTAACATGCACTTTGATTTAAAG 5280
Qy 5281 AACATCTTTCAAGAGCTGTAAGAAATCTACCTGAGGAATCAAAAGAAAGTGTGTTTGG 5340
Db 5281 AACATCTTTCAAGAGCTGTAAGAAATCTACCTGAGGAATCAAAAGAAAGTGTGTTTGG 5340
Qy 5341 CTTTAAAGTATGTAAGGAATCTCTCAGATTTACTTTGCTAGATGAACCACTCTACAGGTATGG 5400
Db 5341 CTTTAAAGTATGTAAGGAATCTCTCAGATTTACTTTGCTAGATGAACCACTCTACAGGTATGG 5400
Qy 5401 ATCCAAAGCCAAACAGACATGTTGGCGAGCAATTCGAACTGCAATTTAAAAACAGAAAGC 5460
Db 5401 ATCCAAAGCCAAACAGACATGTTGGCGAGCAATTCGAACTGCAATTTAAAAACAGAAAGC 5460
Qy 5461 GGGCTGCTATTTCTGACCACTCACTATATGAGAGGAGGAGGCTGCTGCTGATCGAGTAG 5520
Db 5461 GGGCTGCTATTTCTGACCACTCACTATATGAGAGGAGGAGGCTGCTGCTGATCGAGTAG 5520
Qy 5521 CTATCATGCTGCTCTGGGAGTTAAGATGTATCGGAAACAGTACAAATCTTAAAGAGTAAT 5580
Db 5521 CTATCATGCTGCTCTGGGAGTTAAGATGTATCGGAAACAGTACAAATCTTAAAGAGTAAT 5580
Qy 5581 TTGGAAGAGGCTACTTTTGGAAATTTAAATTTGAAGACTGGATAGAAAACCTTAGAAGTAG 5640
Db 5581 TTGGAAGAGGCTACTTTTGGAAATTTAAATTTGAAGACTGGATAGAAAACCTTAGAAGTAG 5640
Qy 5641 ACCGCTTCAAGAGAAATTCAGTATATTTTCCAAATGCAAGCGTCCAGAAAGTTTTT 5700
Db 5641 ACCGCTTCAAGAGAAATTCAGTATATTTTCCAAATGCAAGCGTCCAGAAAGTTTTT 5700
Qy 5701 CTTTCTATTTTGGCTTATATAATTTCTTAAGGAAGATGTTTCACTCCCTTTTCAAACTTTTT 5760
Db 5701 CTTTCTATTTTGGCTTATATAATTTCTTAAGGAAGATGTTTCACTCCCTTTTCAAACTTTTT 5760
Qy 5761 TTAAGCTGGAAGAGCTAAAATCATGCTTTTGGCAATGGAAGATAATAGCTTTTCTCAAGCAA 5820
Db 5761 TTAAGCTGGAAGAGCTAAAATCATGCTTTTGGCAATGGAAGATAATAGCTTTTCTCAAGCAA 5820
Qy 5821 CATTTGAACAGGTTTGTAGAACTCACTAAGAACAGAGAGGAGGAAGATATAGTTCTG 5880
Db 5821 CATTTGAACAGGTTTGTAGAACTCACTAAGAACAGAGAGGAGGAAGATATAGTTCTG 5880
Qy 5881 GAACTTTTAAACAGCACACTTTTGGTGGGAAACGAAACACAGAAAGATAGATTTTGA 5940
Db 5881 GAACTTTTAAACAGCACACTTTTGGTGGGAAACGAAACACAGAAAGATAGATTTTGA 5940
Qy 5941 TTTTGTATTTTGGTCTGCTTACTGGGACTTCTTTTCTTTTCACTTAAATTTTAACTTTGG 6000
Db 5941 TTTTGTATTTTGGTCTGCTTACTGGGACTTCTTTTCTTTTCACTTAAATTTTAACTTTGG 6000
Qy 6001 TTTAAAAAGTTTTTATTTGGAAATGGTAACTGGAGAACCAAGAACGCACTTGAATTTTTC 6060
Db 6001 TTTAAAAAGTTTTTATTTGGAAATGGTAACTGGAGAACCAAGAACGCACTTGAATTTTTC 6060
Qy 6061 TAAAGTCTCTTAAATGAAATGCTGTTGTTGTTGTTTCTTTTCTTTTAAATAAAACGTAT 6120
Db 6061 TAAAGTCTCTTAAATGAAATGCTGTTGTTGTTGTTTCTTTTCTTTTAAATAAAACGTAT 6120
Qy 6121 GTATAATTAAGTGAAGCTGCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 6180
Db 6121 GTATAATTAAGTGAAGCTGCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 6180
Qy 6181 TCATCTTTTTCACCACTTCCAGAACAGTCTTCTGAAATTTGTTGTTGTTGTTGTTGTTGTTG 6240
Db 6181 TCATCTTTTTCACCACTTCCAGAACAGTCTTCTGAAATTTGTTGTTGTTGTTGTTGTTGTTG 6240
Qy 6241 AGAATAGTTTTTATTTTAAAGTTATCTTTAAAGTTTATGCTTCTTAAATAAGTACGTA 6300
Db 6241 AGAATAGTTTTTATTTTAAAGTTATCTTTAAAGTTTATGCTTCTTAAATAAGTACGTA 6300
Qy 6301 ATGTTTCCAACTTAAATAAAAAAACTTAATATCATTAATGCTATGAAAGATACATAAAGC 6360

Db 781 ATTCTGGTCTACCTATTTTCCATGTCCTTGTCTTCTTACCTTTTCCAGAGCTGACAGATTTGCTGCT 840
Qy 841 CCATGCAATTCCTGCTCCAGTTTCTTAAGAGAGACAGCTTTGGATGATGCTTAAATCCATCTTAC 900
Db 841 CCATGCAATTCCTGCTCCAGTTTCTTAAGAGAGACAGCTTTGGATGATGCTTAAATCCATCTTAC 900
Qy 901 CTGGGACTGAACAGCTGCTTATTTTGGCCGTTAAAAATTACATGCAAGTTTACTGCGTGCG 960
Db 901 CTGGGACTGAACAGCTGCTTATTTTGGCCGTTAAAAATTACATGCAAGTTTACTGCGTGCG 960
Qy 961 TCCGGGTTCTTGTGTTGTTTTTCCCTCTTTAAATAGGTTTATTCCAGAAAAATGTCACATG 1020
Db 961 TCCGGGTTCTTGTGTTGTTTTTCCCTCTTTAAATAGGTTTATTCCAGAAAAATGTCACATG 1020
Qy 1021 CAATAGGAGGTAGGATTTGGAGACAGACAGACACTTCTACTGCAAGAAATTTACTTAA 1080
Db 1021 CAATAGGAGGTAGGATTTGGAGACAGACAGACACTTCTACTGCAAGAAATTTACTTAA 1080
Qy 1081 TTAATGTCAGAACCAAAAGAGTAGTGTTCAGGAAATTCCTTTTCCATATTTTTTTTTAT 1140
Db 1081 TTAATGTCAGAACCAAAAGAGTAGTGTTCAGGAAATTCCTTTTCCATATTTTTTTTTAT 1140
Qy 1141 TTTGGTTAATTAATTAATAGCATGATGATCCAAATAGAAATATGAAGATGCTCCTAATA 1200
Db 1141 TTTGGTTAATTAATTAATAGCATGATGATCCAAATAGAAATATGAAGATGCTCCTAATA 1200
Qy 1201 TAGAATCAATCCTATGGACAAAGTTTACTCTTCTTAATCTAAATCTTTGGATATACTCCAG 1260
Db 1201 TAGAATCAATCCTATGGACAAAGTTTACTCTTCTTAATCTAAATCTTTGGATATACTCCAG 1260
Qy 1261 TGACTTAATTAACAGCAGATCATGAGAAAGTGTCTACTGATCATCTACCTGATGTCA 1320
Db 1261 TGACTTAATTAACAGCAGATCATGAGAAAGTGTCTACTGATCATCTACCTGATGTCA 1320
Qy 1321 TAAATCTGAAGATATACAAATGAAAGAAATGTTTAAATCCAGTCTCTCTAAGCCGA 1380
Db 1321 TAAATCTGAAGATATACAAATGAAAGAAATGTTTAAATCCAGTCTCTCTAAGCCGA 1380
Qy 1381 GCAATTTGTAGGTGCTGTTTCAAGACCTCCATGCTCTATGATCACTTCTTTTCTG 1440
Db 1381 GCAATTTGTAGGTGCTGTTTCAAGACCTCCATGCTCTATGATCACTTCTTTTCTG 1440
Qy 1441 ATATGATTCAGATATCTTCTATTTATATGATGATCAAGAGCTGCTGTTTCAAAATCATGTG 1500
Db 1441 ATATGATTCAGATATCTTCTATTTATATGATGATCAAGAGCTGCTGTTTCAAAATCATGTG 1500
Qy 1501 AGGCTGCTCAGTACTGCTGCTCCTCAGGTTTTCAGGTTTTCAGATCCATAGATGCTGCCA 1560
Db 1501 AGGCTGCTCAGTACTGCTGCTCCTCAGGTTTTCAGGTTTTCAGATCCATAGATGCTGCCA 1560
Qy 1561 TTATACAGTTGAAGACCAATGTTTCTCTTTGGAGGAGCTGGAGTCAACTTAAAGCTGTTA 1620
Db 1561 TTATACAGTTGAAGACCAATGTTTCTCTTTGGAGGAGCTGGAGTCAACTTAAAGCTGTTA 1620
Qy 1621 TTATGGAGAACTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTAAATTTAATAT 1680
Db 1621 TTATGGAGAACTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTAAATTTAATAT 1680
Qy 1681 ACCTAGTTATAGCAATTTTCCACTTTTGGATACCTTTTGGCAATTCATATGCTAGCAGAAA 1740
Db 1681 ACCTAGTTATAGCAATTTTCCACTTTTGGATACCTTTTGGCAATTCATATGCTAGCAGAAA 1740
Qy 1741 AAGAAAAAATAAAGAAATTTTAAAGATAATAGGACCTTCATGATACCTGCTTTTGGC 1800
Db 1741 AAGAAAAAATAAAGAAATTTTAAAGATAATAGGACCTTCATGATACCTGCTTTTGGC 1800
Qy 1801 TTTCTGGGTTCTTCTATATACAGTTTAAATTTTCTTATGCTCCCTTCTTATGCGAGTCA 1860
Db 1801 TTTCTGGGTTCTTCTATATACAGTTTAAATTTTCTTATGCTCCCTTCTTATGCGAGTCA 1860
Qy 1861 TTGCGACAGCTTCTTTGTATTTCTCCTCAAAAGTAGCAGATGATGATTTTCTGCTTTTTT 1920
Db 1861 TTGCGACAGCTTCTTTGTATTTCTCCTCAAAAGTAGCAGATGATGATTTTCTGCTTTTTT 1920

Qy 1921 TCCTTTATGGATTATCATCTGTAATTTTTTGTCTTTAATGCTGACACCTCTTTTAAAAAAT 1980
Db 1921 TCCTTTATGGATTATCATCTGTAATTTTTTGTCTTTAAATGCTGACACCTCTTTTAAAAAAT 1980
Qy 1981 CAAAACATGTGGGAATAGTTGAAATTTTTTGTACTGTGGCTTTTGGATTTATG3CCTTA 2040
Db 1981 CAAAACATGTGGGAATAGTTGAAATTTTTTGTACTGTGGCTTTTGGATTTATG3CCTTA 2040
Qy 2041 TGATTAATCCTCATAGAAAGTTTCCCAAAATCGTTAGTGTGGCTTTTCAAGTCTTCTCTGC 2100
Db 2041 TGATTAATCCTCATAGAAAGTTTCCCAAAATCGTTAGTGTGGCTTTTCAAGTCTTCTCTGC 2100
Qy 2101 ACTGTACTTTTGTGATTTGATTTGACAGAGTTCATGCAATTTAGAAATTTAATGAAGGTG 2160
Db 2101 ACTGTACTTTTGTGATTTGATTTGACAGAGTTCATGCAATTTAGAAATTTAATGAAGGTG 2160
Qy 2161 CTTCAATTTTCAAAATTTGACTGCGAGGCCCATATCTCTCTAAATTTATTAACAATTTATCATGCTCA 2220
Db 2161 CTTCAATTTTCAAAATTTGACTGCGAGGCCCATATCTCTCTAAATTTATTAACAATTTATCATGCTCA 2220
Qy 2221 CACTTAATAGTATATTTCTATGTCCTCTTGGCTGTCTATCTTGAAGCCTTCATATTTGGTCAAGAGTA 2280
Db 2221 CACTTAATAGTATATTTCTATGTCCTCTTGGCTGTCTATCTTGAAGCCTTCATATTTGGTCAAGAGTA 2280
Qy 2281 AATTTGGCTTTACGAGATCATCTTTATATTTTCTGAAGCCTTCATATTTGGTCAAGAGTA 2340
Db 2281 AATTTGGCTTTACGAGATCATCTTTATATTTTCTGAAGCCTTCATATTTGGTCAAGAGTA 2340
Qy 2341 AAAAGAAATTTATGAGGATTTATCAGAGGCCAATGTTTAAATGGAATTTAGTTTGTAGTAAA 2400
Db 2341 AAAAGAAATTTATGAGGATTTATCAGAGGCCAATGTTTAAATGGAATTTAGTTTGTAGTAAA 2400
Qy 2401 TTATTTGAGCCAGTTTCTTCAGAAATTTGTAGAAAGAGCCATAGAAATTTAGTGTATTC 2460
Db 2401 TTATTTGAGCCAGTTTCTTCAGAAATTTGTAGAAAGAGCCATAGAAATTTAGTGTATTC 2460
Qy 2461 AGAAGACATACAGAAAGAGGTTGAAATGTTGAGGCTTTGAGAAATTTGTCAATTTGACA 2520
Db 2461 AGAAGACATACAGAAAGAGGTTGAAATGTTGAGGCTTTGAGAAATTTGTCAATTTGACA 2520
Qy 2521 TATATGAGGCTCAGATTTACTGCTTTACTGCGCCACAGTGGCAACAGAGAGAGTACATTTGA 2580
Db 2521 TATATGAGGCTCAGATTTACTGCTTTACTGCGCCACAGTGGCAACAGAGAGAGTACATTTGA 2580
Qy 2581 TGAATATTTCTTTGTGGACTCTGCCCACTTCTGATGGGTTTGCATCTATATATGACACA 2640
Db 2581 TGAATATTTCTTTGTGGACTCTGCCCACTTCTGATGGGTTTGCATCTATATATGACACA 2640
Qy 2641 GAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATTTGGCATTGTTCCACAGT 2700
Db 2641 GAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATTTGGCATTGTTCCACAGT 2700
Qy 2701 TAGATATACACTTTGATGCTTTTGAAGTAGAAGAAAAATTTATCAATTTTGGCTTCAATCA 2760
Db 2701 TAGATATACACTTTGATGCTTTTGAAGTAGAAGAAAAATTTATCAATTTTGGCTTCAATCA 2760
Qy 2761 AAGGATACCGCCCAACAAATATATAACAAGAGTGCAGAGGTTTTTACTAGATTTTAGACA 2820
Db 2761 AAGGATACCGCCCAACAAATATATAACAAGAGTGCAGAGGTTTTTACTAGATTTTAGACA 2820
Qy 2821 TGCAGACTATCAAGATTAACCAAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2880
Db 2821 TGCAGACTATCAAGATTAACCAAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2880
Qy 2881 CATTAGGAATTCCTGTTCTTTGGGAAACCCCAAGATGCTGCTAGATGAACCAAGCTG 2940
Db 2881 CATTAGGAATTCCTGTTCTTTGGGAAACCCCAAGATGCTGCTAGATGAACCAAGCTG 2940
Qy 2941 GAATGACCCCTGTTCTCGACATATTTGATGAAATCTTTTAAATACAGAAAGCCAAATC 3000
Db 2941 GAATGACCCCTGTTCTCGACATATTTGATGAAATCTTTTAAATACAGAAAGCCAAATC 3000

Qy	3001	GGGTGACAGTGTTCAGTACTCAATTTTCATGGATGAAGTCGACATTTCTTGCAGATAGGAAG	3060
Db	3001	GGGTGACAGTGTTCAGTACTCAATTTTCATGGATGAAGTCGACATTTCTTGCAGATAGGAAG	3060
Qy	3061	CTGTGATATCAACAGGAATGCTGAATGTGTGGTTCTTCAATGTTCTCTAAAAAGTAAAT	3120
Db	3061	CTGTGATATCAACAGGAATGCTGAATGTGTGGTTCTTCAATGTTCTCTCAAAATGTAAT	3120
Qy	3121	GGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATGTGGCCACAGAAATCTCTTT	3180
Db	3121	GGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATGTGGCCACAGAAATCTCTTT	3180
Qy	3181	CTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATATACACAGAAATGACCAACAAC	3240
Db	3181	CTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATATACACAGAAATGACCAACAAC	3240
Qy	3241	TTGTGTATAGCTTGCCTTTCAAGACATGGACAAATTTTCAGGTTTGTGTTCTGCCCCTAG	3300
Db	3241	TTGTGTATAGCTTGCCTTTCAAGACATGGACAAATTTTCAGGTTTGTGTTCTGCCCCTAG	3300
Qy	3301	ACAGTCATTCAAATTTGGGTGTCATTTCTTATGGTGTGTTTCATGACACATTTTGGAGACGC	3360
Db	3301	ACAGTCATTCAAATTTGGGTGTCATTTCTTATGGTGTGTTTCATGACACATTTTGGAGACGC	3360
Qy	3361	TATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATATATAGTGTATTTTACTC	3420
Db	3361	TATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATATATAGTGTATTTTACTC	3420
Qy	3421	AGCAGCCACTGGAGAGAAATGATTCAAATCTTTTGTATGAATGGAAACAGAGCTTAC	3480
Db	3421	AGCAGCCACTGGAGAGAAATGATTCAAATCTTTTGTATGAATGGAAACAGAGCTTAC	3480
Qy	3481	TTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGCAAAACAACAGA	3540
Db	3481	TTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGCAAAACAACAGA	3540
Qy	3541	TGTATACAAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGCTGAAAGTAAATCAGTGAGAT	3600
Db	3541	TGTATACAAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGCTGAAAGTAAATCAGTGAGAT	3600
Qy	3601	CAGTGTGCTTCGCTTTTAAATTTTTTTCACAGTTCAGATTTTTTATGTTTTTGTTGGTTCATC	3660
Db	3601	CAGTGTGCTTCGCTTTTAAATTTTTTTCACAGTTCAGATTTTTTATGTTTTTGTTGGTTCATC	3660
Qy	3661	ACTCTTTTAAAAATGCTGTGGTCCCATCAAACTTGTTCCAGACTTATATTTTTCTATAAAC	3720
Db	3661	ACTCTTTTAAAAATGCTGTGGTCCCATCAAACTTGTTCCAGACTTATATTTTTCTATAAAC	3720
Qy	3721	CTGAGACAAACCAATAAATAACAAACAAAGTCTGCTTTCTTCAAAATTCCTGCTGACTCAG	3780
Db	3721	CTGAGACAAACCAATAAATAACAAACAAAGTCTGCTTTCTTCAAAATTCCTGCTGACTCAG	3780
Qy	3781	ATATCAGTGATCTTATTAGCTTTTTCACAGCCAGAACATATGTTGGTGAGATTAATG	3840
Db	3781	ATATCAGTGATCTTATTAGCTTTTTCACAGCCAGAACATATGTTGGTGAGATTAATG	3840
Qy	3841	ACAGTGACTATGATCCGTGGCTCCCATAGTCGGCTTTTAAATGTGATGCAATTCAGAAA	3900
Db	3841	ACAGTGACTATGATCCGTGGCTCCCATAGTCGGCTTTTAAATGTGATGCAATTCAGAAA	3900
Qy	3901	AGGACTATGTTTTGACGCTGTTTTCAACAGTACTATGGTTTATCTTTTACCTATATATAG	3960
Db	3901	AGGACTATGTTTTGACGCTGTTTTCAACAGTACTATGGTTTATCTTTTACCTATATATAG	3960
Qy	3961	TGAATATCATTAGTAAGTACTATCTTTATCATTTAAATGTGACTGAAAACATCCAGATCT	4020
Db	3961	TGAATATCATTAGTAAGTACTATCTTTATCATTTAAATGTGACTGAAAACATCCAGATCT	4020
Qy	4021	GGAGTACCCCATTTCTTCAAGAAATTAAGTATAGTTTTTAAAAATGTAGCTGTAATTTTC	4080
Db	4021	GGAGTACCCCATTTCTTCAAGAAATTAAGTATAGTTTTTAAAAATGTAGCTGTAATTTTC	4080
Qy	4081	AAGCAGCTTTGCTTGGAAATCATTGTTACTGCAATGCCACTTACTTTTGCATGGAAAAATG	4140

Db	4081	 AAGCAGCTTTGCTTGGATCAATGTGTACTGCAATGCCACCTTACTTTGGCCATGAAAAATG	4140
Qy	4141	CAGAGAATCATAAAGATCAAAAGCTTTATCTCAACTTAAACCTTTCAGGTCCTTTGCCATCTG	4200
Db	4141	CAGAGAACTATAAGATCAAAAGCTTTATCTCAACTTAAACCTTTCAGGTCCTTTGGCCATCTG	4200
Qy	4201	CATATPGGATTTGGACAAGCTGTGTTGATATCCCTTTATTTTTATCATTTCTATTTTGA	4260
Db	4201	CATATPGGATTTGGACAAGCTGTGTTGATATCCCTTTATTTTTATCATTTCTATTTTGA	4260
Qy	4261	TGCTAGGAAGCTTACTGGCAATTCATTTATGGATTATATTTTTATCTGTAAGAGTTCCTTG	4320
Db	4261	TGCTAGGAAGCTTACTGGCAATTCATTTATGGATTATATTTTTATCTGTAAGAGTTCCTTG	4320
Qy	4321	CTGTGGTTTTTTTGGCTTATTGTTTATGTTCCATCAGTTATTTCTGTGTCACATTATATGCTT	4380
Db	4321	CTGTGGTTTTTTTGGCTTATTGTTTATGTTCCATCAGTTATTTCTGTGTCACATTATATGCTT	4380
Qy	4381	CTTTCACTTTAAGAAAAATTTAAATACCAAGAAATTTTGGTCATTTATCTATCTGTGTGG	4440
Db	4381	CTTTCACTTTTAAAGAAAAATTTAAATACCAAGAAATTTTGGTCATTTATCTATCTGTGTGG	4440
Qy	4441	CAGGGTTGNCCTTGTATTGCAATCACTGAAATAAAGCTTTCTTTATGGGATACAAATTCGAA	4500
Db	4441	CAGGGTTGNCCTTGTATTGCAATCACTGAAATAAAGCTTTCTTTATGGGATACAAATTCGAA	4500
Qy	4501	CTATTTCTTCAATGTCCTTTTGTATCATCAATCCATCTATCCACTCTAGGTTGCTGTA	4560
Db	4501	CTATTTCTTCAATGTCCTTTTGTATCATCAATCCATCTATCCACTCTAGGTTGCTGTA	4560
Qy	4561	TTTTCTTTCAATAAGATTTCTTTGGAAGAAATGTACGAAAAATGTGGACACCTATAATCCAT	4620
Db	4561	TTTTCTTTCAATAAGATTTCTTTGGAAGAAATGTACGAAAAATGTGGACACCTATAATCCAT	4620
Qy	4621	GGGATAGGCTTTTCACTAGCTGTGTATATCGCCTTTACCTGCAAGTGTACTGTGATTTTCC	4680
Db	4621	GGGATAGGCTTTTCACTAGCTGTGTATATCGCCTTTACCTGCAAGTGTACTGTGATTTTCC	4680
Qy	4681	TCCTTACAATACTATGAGAAAAATATGGAGGCAGATCAATAGAAAAAGATCCCTTTTTTCA	4740
Db	4681	TCCTTACAATACTATGAGAAAAATATGGAGGCAGATCAATAGAAAAAGATCCCTTTTTTCA	4740
Qy	4741	GAACCTTTTCAACGAAGCTTAAAAATAGGAAGCTTCCAGAACCAACCAGACAATGAGGATG	4800
Db	4741	GAACCTTTTCAACGAAGCTTAAAAATAGGAAGCTTCCAGAACCAACCAGACAATGAGGATG	4800
Qy	4801	AAGATGAAGATGTCAAAGCTGAAAAGACTAAAGTCAAAGAGCTGATGGGTGCCAGTGT	4860
Db	4801	AAGATGAAGATGTCAAAGCTGAAAAGACTAAAGTCAAAGAGCTGATGGGTGCCAGTGT	4860
Qy	4861	GTGAGGAGAAACCATCCATTTATGGTCAGCAATTTGCTAATAAGAAATATGATGACAAGAAAG	4920
Db	4861	GTGAGGAGAAACCATCCATTTATGGTCAGCAATTTGCTAATAAGAAATATGATGACAAGAAAG	4920
Qy	4921	ATTTTCTTTTCAAGAAAAAGTAAAGAAAGTGCAACTAAATACATCTCTTTCTGTGTGA	4980
Db	4921	ATTTTCTTTTCAAGAAAAAGTAAAGAAAGTGCAACTAAATACATCTCTTTCTGTGTGA	4980
Qy	4981	AAAAAGAGAGATCTTTAGGACTATTGGGTCCAAATGGTGTCTGGCAAAAGCACAATTTA	5040
Db	4981	AAAAAGAGAGATCTTTAGGACTATTGGGTCCAAATGGTGTCTGGCAAAAGCACAATTTA	5040
Qy	5041	ATATTTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGATTTTTTAGAGATTAATCTT	5100
Db	5041	ATATTTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGATTTTTTAGAGATTAATCTT	5100
Qy	5101	CAGAGACAAGTGAAGATGATGTTTCACTCAAGTGTATGGTTTACTGTCTCAGATAAACC	5160
Db	5101	CAGAGACAAGTGAAGATGATGTTTCACTCAAGTGTATGGTTTACTGTCTCAGATAAACC	5160
Qy	5161	CTTTGTGGCCAGATCACTAATTCAGGAAACATTTTTGAAATTTATGGAGCTGTCAAAGGAA	5220
Db	5161	CTTTGTGGCCAGATCACTAATTCAGGAAACATTTTTGAAATTTATGGAGCTGTCAAAGGAA	5220

Db 528 TCCTTCTATTGTTCCCTCTTCTACTTTTGTCTCCCTGGCTGCTGTTTCTTATCCTCC 587
Qy 361 AGCCAGAGACTAGTGTATTTTCTCCTATGTTGTATACACACTTGTGCAGCTGCAACCAC 420
Db 588 AGCCAGAGACTAGTGTATTTTCTCCTATGTTGTATACACACTTGTGCAGCTGCAACCAC 647
Qy 421 CATATCCAGGCCCAATGGTAGGAGGTAGAGAAAGAAAGCAAAAGGGAATGGCTCATCC 480
Db 648 CATATCCAGGCCCAATGGTAGGAGGTAGAGAAAGAAAGCAAAAGGGAATGGCTCATCC 707
Qy 481 TCTTACACCATAGTTCATGTAATAGAGAGAAAGGTTTCTCCCTCAGAGTGTGGCT 540
Db 708 TCTTACACCATAGTTCATGTAATAGAGAGAAAGGTTTCTCCCTCAGAGTGTGGCT 767
Qy 541 GCACTAGGCTTTTGTACTGTAGTCTGCCCTGTTCACATGGGATGCTTGCATGTGGGG 600
Db 768 GCACTAGGCTTTTGTACTGTAGTCTGCCCTGTTCACATGGGATGCTTGCATGTGGGG 827
Qy 601 ATACAGAGAAATCAGAAAAAGAAAAAGATTTGCTATFTTCTACATFTCTCCCTGAGCAAT 660
Db 828 ATACAGAGAAATCAGAAAAAGAAAAAGATTTGCTATFTTCTACATFTCTCCCTGAGCAAT 887
Qy 661 AAGACCTCCCTGCCATTCCTCAATTCAAAGCTTAAGGCTTCTCTGGAGCTGCCCTGT 720
Db 888 AAGACTTCCCTTGCCCAATTCCTCAATTCAAAGCTTAAGGCTTCTCTGGAGCTGCCCTGT 947
Qy 721 GGGCGGTTCCGGAGATACCAAAGAGAAAAAGTACCACCTGTGATATGGTGTATTTCAA 780
Db 948 GGGCGGTTCCGGAGATACCAAAGAGAAAAAGTACCACCTGTGATATGGTGTATTTCAA 1007
Qy 781 ATTCTGGTCTACCCATTTTCCACATGCCCTGTGTTTACTTTTTCAGAGCTGACAGATTTGCTGT 840
Db 1008 ATTCTGGTCTACCCATTTTCCACATGCCCTGTGTTTACTTTTTCAGAGCTGACAGATTTGCTGT 1067
Qy 841 CCATGCATTCCTGCCAGTTTCTTAAGAGAGACAGCTGGAGTATGCTTAATCCATCTTAC 900
Db 1068 CCATGCATTCCTGCCAGTTTCTTAAGAGAGACAGCTGGAGTATGCTTAATCCATCTTAC 1127
Qy 901 CTGGGACTGAAACAGCTGCTTATTTTCCGTTAAAAATACATGCAGTTTACTCGCTGGC 960
Db 1128 CTGGGACTGAAACAGCTGCTTATTTTCCGTTAAAAATACATGCAGTTTACTCGCTGGC 1187
Qy 961 TCCGGGTTGTTGTTGTTGTTTCTCTTTAATAGGTTTATTCAGAAAAATGCTCCACTG 1020
Db 1188 TCCGGGTTGTTGTTGTTGTTTCTCTTTAATAGGTTTATTCAGAAAAATGCTCCACTG 1247
Qy 1021 CAATTAGGGAGGTAGGAGTTTGGAGACAGACCAAGAACATCTTCTAAGAAATTTACTTAA 1080
Db 1248 CAATTAGGGAGGTAGGAGTTTGGAGACAGACCAAGAACATCTTCTAAGAAATTTACTTAA 1307
Qy 1081 TTAATAGCAGAACCAAAAGAGTAGTGTTCAGGAAATTTCTTCCACTATTTTCTTAT 1140
Db 1308 TTAATAGCAGAACCAAAAGAGTAGTGTTCAGGAAATTTCTTCCACTATTTTCTTAT 1367
Qy 1141 TTTGGTTTAATTAATTAGCATGATGCATCCAAATAGAAATATGAAGAGTGCCTAATA 1200
Db 1368 TTTGGTTTAATTAATTAGCATGATGCATCCAAATAGAAATATGAAGAGTGCCTAATA 1427
Qy 1201 TAGAACTCAATCCTATGGGACAGTTTACTCTTTCTAATCTAATTTCTTGGATATACTCCAG 1260
Db 1428 TAGAACTCAATCCTATGGGACAGTTTACTCTTTCTAATCTAATTTCTTGGATATACTCCAG 1487
Qy 1261 TGACTAATATTAAGCAGCATCATCAGAAAGTGTCTACTGATCATCTACTCTGATGTCA 1320
Db 1488 TGACTAATATTAAGCAGCATCATCAGAAAGTGTCTACTGATCATCTACTCTGATGTCA 1547
Qy 1321 TAAATTACTGAAGAATATACAAATGAAAAAGAAATGTTTAAATCCAGTCTCTCTAAGCCGA 1380
Db 1548 TAAATTACTGAAGAATATACAAATGAAAAAGAAATGTTTAAATCCAGTCTCTCTAAGCCGA 1607
Qy 1381 GCAACTTTGTAGGTGGTTTTTCAAAGACTCCATGTCTCTATGAACCTTCGTTTTTCTCTG 1440
Db 1608 GCAACTTTGTAGGTGGTTTTTCAAAGACTCCATGTCTCTATGAACCTTCGTTTTTCTCTG 1667

Qy 1441 AVATGATTCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTTCAAAAATCATGTG 1500
Db 1668 AVATGATTCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTTCAAAAATCATGTG 1727
Qy 1501 AGGCTGCTCAGTACTGGTCTCCTCAGGTTTTCACAGTTTTCACAGCATCCATAGATGTGCCA 1560
Db 1728 AGGCTGCTCAGTACTGGTCTCCTCAGGTTTTCACAGTTTTCACAGCATCCATAGATGTGCCA 1787
Qy 1561 TTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACTAAAGCTGTGTA 1620
Db 1788 TTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACTAAAGCTGTGTA 1847
Qy 1621 TTATGGGAGAAATCGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTAAATTTTAAATAT 1680
Db 1848 TTATGGGAGAAATCGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTAAATTTTAAATAT 1907
Qy 1681 ACCTAGTTATAGCAATTTTCCCTTTTGGATATCTTTTGGCAATTCATATCGTAGCAGAAA 1740
Db 1908 ACCTAGTTATAGCAATTTTCCCTTTTGGATATCTTTTGGCAATTCATATCGTAGCAGAAA 1967
Qy 1741 AAGAAAAAAATPAAAAAGAAATTTTAAAGATATAGGACTTTCATGATACCTCTTTTGGC 1800
Db 1968 AAGAAAAAAATPAAAAAGAAATTTTAAAGATATAGGACTTTCATGATACCTCTTTTGGC 2027
Qy 1801 TTTTCTGGGTTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCCTTTCTTATGGCAGTCA 1860
Db 2028 TTTTCTGGGTTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCCTTTCTTATGGCAGTCA 2087
Qy 1861 TTGCGACAGCTTCTTTGTTTATTTCTTCAAGTAGCAGCATTTGTGATATTTCTGCTTTTTT 1920
Db 2088 TTGCGACAGCTTCTTTGTTTATTTCTTCAAGTAGCAGCATTTGTGATATTTCTGCTTTTT 2147
Qy 1921 TCCCTTATGGATATCATCTGTATTTTCTTAAATGCTGACACCTCTTTTAAAAAAT 1980
Db 2148 TCCCTTATGGATATCATCTGTATTTTCTTAAATGCTGACACCTCTTTTAAAAAAT 2207
Qy 1981 CAAAAATGTTGGAAATAGTTTGAATTTTGTACTGTGGCTTTTGGATTTTATTTGGCCTTA 2040
Db 2208 CAAAAATGTTGGAAATAGTTTGAATTTTGTACTGTGGCTTTTGGATTTTATTTGGCCTTA 2267
Qy 2041 TGATAATCCTCATPAGAAAGTTTCCCAATCGTTAGTGTGGCTTTTCAAGTCTTTCTGTC 2100
Db 2268 TGATAATCCTCATPAGAAAGTTTCCCAATCGTTAGTGTGGCTTTTCAAGTCTTTCTGTC 2327
Qy 2101 ACTGTACTTTTGTGATTTGTATTTGACAGGTCTATGATTTTAGAAGATTTTAAAGAAGTG 2160
Db 2328 ACTGTACTTTTGTGATTTGTATTTGCAAGGTCTATGCAAGGTCTTTTAAAGAAGTG 2387
Qy 2161 CTTTCAATTTCAAAATTTGACTGCGAGGCCCATATCTCTAAATTTTACAAATTTATCATGTCA 2220
Db 2388 CTTTCAATTTCAAAATTTGACTGCGAGGCCCATATCTCTAAATTTTACAAATTTATCATGTCA 2447
Qy 2221 CACTTAAATAGTATPATTTCTATGTCTCTTGGCTGTATCTTGTATCAAGTCAATTCAGGGG 2280
Db 2448 CACTTAAATAGTATPATTTCTATGTCTCTTGGCTGTATCTTGTATCAAGTCAATTCAGGGG 2507
Qy 2281 AATTGGCTTACGGAGATCATCTTTATATTTTCTGAGCCCTCATATTTGTGTCAGAGTGA 2340
Db 2508 AATTGGCTTACGGAGATCATCTTTATATTTTCTGAGCCCTCATATTTGTGTCAGAGTGA 2567
Qy 2341 AAAGAAATTTATGAGGAGTTTATCAGAGGCCAATGTTAATGGAATATTTAGTTTGTAGTAAA 2400
Db 2568 AAAGAAATTTATGAGGAGTTTATCAGAGGCCAATGTTAATGGAATATTTAGTTTGTAGTAAA 2627
Qy 2401 TTATTGAGCCAGTTTCTTCTCAGAAATTTGTAGGAAAAAGGCCATTAAGAATTTAGTGTATTC 2460
Db 2628 TTATTGAGCCAGTTTCTTCTCAGAAATTTGTAGGAAAAAGGCCATTAAGAATTTAGTGTATTC 2687
Qy 2461 AGAAGACATACAGAAAGAGGGTGAATAATGTGGAGGCTTTGAGAAATTTGTCTCATTTTGACA 2520
Db 2688 AGAAGACATACAGAAAGAGGGTGAATAATGTGGAGGCTTTGAGAAATTTGTCTCATTTTGACA 2747


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Db 4908 TCCTTACAATCTATGAGAAAAAATATGAGGCGAGATCAATAAGAAAAAGATCCCTTTTCA 4967
Qy 4741 GAAACCTTTTCAAGCAAGCTCTAAAAATAGGAAGCTTCCAGAACACACAGACAAATGAGGATG 4800
Db 4968 GAAACCTTTTCAAGCAAGCTCTAAAAATAGGAAGCTTCCAGAACACACAGACAAATGAGGATG 5027
Qy 4801 AAGATGAAGATGTCAAAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGTTCAGGTGTT 4860
Db 5028 AAGATGAAGATGTCAAAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGTTCAGGTGTT 5087
Qy 4861 GTGAGGAGAAACCAATCATTTATGGTCAGCAATTTGCAATAAGATATGATGACAGAAAG 4920
Db 5088 GTGAGGAGAAACCAATCATTTATGGTCAGCAATTTGCAATAAGATATGATGACAGAAAG 5147
Qy 4921 ATTTTCTTTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTGTGA 4980
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Qy 4981 AAAAAAGAGAGATCTTTAGGACTATTTGGGTCAAATGGTCTGGCAAAAGCACAATATTA 5040
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Qy 5041 ATATTCTGGTGTGTGATTTGAACCAACTTTCAGGCCAGGTATTTTAGGAGATATTCIT 5100
Db 5268 ATATTCTGGTGTGTGATTTGAACCAACTTTCAGGCCAGGTATTTTAGGAGATATTCIT 5327
Qy 5101 CAGAGACAAGTGAAGATGATGATTTCACTGAAGTGTATGGGTACTGTCTCAGATAAAC 5160
Db 5328 CAGAGACAAGTGAAGATGATGATTTCACTGAAGTGTATGGGTACTGTCTCAGATAAAC 5387
Qy 5161 CTTTGTGGCCAGATPACTACATTCAGGAACATTTTGAATTTTATGGAGCTGTCAAAAGGAA 5220
Db 5388 CTTTGTGGCCAGATPACTACATTCAGGAACATTTTGAATTTTATGGAGCTGTCAAAAGGAA 5447
Qy 5221 TGAGTGAAGTGAATGATGATGATTAAGTGAATGATGATGATGATGATGATGATGATGAT 5280
Db 5448 TGAGTGAAGTGAATGATGATGATTAAGTGAATGATGATGATGATGATGATGATGATGAT 5507
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DEFINITION Sequence 4 from Patent WO02070690.
ACCESSION AX537473
VERSION AX537473.1 GI:25269282
KEYWORDS Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Chen, H., Kilinski, L. and le Bihan, S.
TITLE Abca5 transporter and uses thereof
JOURNAL Patent: WO 02070690-A 4 12-SEP-2002;
Active Pass Pharmaceuticals, Inc. (CA)
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Matches 5375; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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DEFINITION Sequence 1 from Patent W002070690.
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VERSION AX537470.1 GI:25269277
KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Chen, H., Kilinski, L. and le Bihan, S.
AUTHORS Abca5 transporter and uses thereof
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Best Local Similarity 98.9%; Pred. No. 0;
Matches 5340; Conservative 0; Mismatches 8; Indels 50; Gaps 3;
QY 994 AGGTTTATTCAGAAACATGTCACATGCAATTTAGGGAGGTAGGAGTTTGGAGACAGACCA 1053
Db 97 AGGTTTATTCAGAAACATGTCACATGCAATTTAGGGAGGTAGGAGTTTGGAGACAGACCA 156
QY 1054 GAACACTTCTACTGAGAAATTTACTTTAAATGAGAACCAAAAGAGTAGTGTTCAGG 1113
Db 157 GAACACTTCTACTGAGAAATTTACTTTAAATGAGAACCAAAAGAGTAGTGTTCAGG 216
QY 1114 AAATTTCTTTTCCACTATTTTATTTTGGTTAAATTAATTAAGCATGATGTCATCAA 1173
Db 217 AAATTTCTTTTCCACTATTTTATTTTGGTTAAATTAATTAAGCATGATGTCATCAA 276
QY 1174 ATAAGAAATATGAAGAGTGCTTAATATAGAACTCAATCCATATGAGCAAGTTTACTCTTT 1233
Db 277 ATAAGAAATATGAAGAGTGCTTAATATAGAACTCAATCCATATGAGCAAGTTTACTCTTT 336
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Db 397 TGCTTACTGATCATCTCTACTGATGTCAATAATTACTGAAAGAAATATACAAATGAAAAAGAAA 456
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Db 457 TGTTAAACATCCAGTCTCTCTAAAGCCGAGCAACTTTGTAGGTGTGTTTTCAAGACTCCA 516
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Db 517 TGCTCTATGAACTTCGTTTTTCTCGATATGATTTCCAGTATCTTCTATTTATATGGAAT 576
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QY 1594 AGGAGCTGGAGTCAACTAAAGCTGTTTATGAGGAGAACTGCTGTTGTAGAAATAGATA 1653
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QY 1654 CTTTTCCTCCGAGGAGTAATTTTAAATATACCTAGTTTATAGCATTTTTCACCTTTTGGATACT 1713
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QY 1774 TGGGACTTCATGATATCTGCTTTTGGCTTTCTGAGGTTCTTCTATATACAGTTTAAATTT 1833
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QY	2074	TAGTGTGGCTTTTTCAGTCCCTTCTGTGACGTACTTTTGTGATTTGGTATGACAGGTCA	2133
Db	1177	TAGTGTGGCTTTTTCAGTCCCTTCTGTGACGTACTTTTGTGATTTGGTATGACAGGTCA	1236
QY	2134	TGCATTTAGAAAGATTTTAAATGAAGGTGCTTCATTTTCAAAATTTGACTGCAAGGCCATATC	2193
Db	1237	TGCATTTAGAAAGATTTTAAATGAAGGTGCTTCATTTTCAAAATTTGACTGCAAGGCCATATC	1296
QY	2194	CTCTAATTTATACAAATTTATCATGCTCACATTAATAGTATATTTCTATGTCCTCTGGCTG	2253
Db	1297	CTCTAATTTATACAAATTTATCATGCTCACATTAATAGTATATTTCTATGTCCTCTGGCTG	1356
QY	2254	TCATCTTTGATCAAGTCATTTCCAGGGGAATTTGGCTTACGGAGTCAATCTTTATATTTTC	2313
Db	1357	TCATCTTTGATCAAGTCATTTCCAGGGGAATTTGGCTTACGGAGTCAATCTTTATATTTTC	1416
QY	2314	TGAAGCCTTCATATTTGGTCAAGAGTAAAGAAATTTATGAGGAGTTTATCAGAGGGCAATG	2373
Db	1417	TGAAGCCTTCATATTTGGTCAAGAGTAAAGAAATTTATGAGGAGTTTATCAGAGGGCAATG	1476
QY	2374	TTAATGGAAATATTTAGTTTGTAGTAAATTTAGGCCAGTTTCTTCAGAAATTTGTAGGAA	2433
Db	1477	TTAATGGAAATATTTAGTTTGTAGTAAATTTAGGCCAGTTTCTTCAGAAATTTGTAGGAA	1536
QY	2434	AAGAGCCATAAGAAATTTAGTGGTATTTCCAGAAGCATACAGAAAGAGGGTGAANAATGTGG	2493
Db	1537	AAGAGCCATAAGAAATTTAGTGGTATTTCCAGAAGCATACAGAAAGAGGGTGAANAATGTGG	1596
QY	2494	AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAGATTTACTGCCCTTACTTGGCC	2553
Db	1597	AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAGATTTACTGCCCTTACTTGGCC	1656
QY	2554	ACAGTGGAAACAGAAAGAGTACATTTGATGAATATTTCTTTGTGACCTCTGC-CCACCTTCTG	2613
Db	1657	ACAGTGGAAACAGAAAGAGTACATTTGATGAATATTTCTTTGTGACCTCTGC-CCACCTTCTG	1716
QY	2614	ATGGGTTTGACATCTATATATGGAACACAGAGTCTCAGAAATAGATGAATTTTGAAGCAA	2673
Db	1717	ATGGGTTTGACATCTATATATGGAACACAGAGTCTCAGAAATAGATGAATTTTGAAGCAA	1776
QY	2674	GAANAATGATTTGGCATTTTGCACAGTTAGATATACACTTTTGATTTTTCACACAGTAGAAG	2733
Db	1777	GAANAATGATTTGGCATTTTGCACAGTTAGATATACACTTTTGATTTTTCACACAGTAGAAG	1836
QY	2734	AAAATTTATCAAATTTTGGCTTCAATCAAAGGGATACAGGCAACAATATATATACAAGAAG	2793
Db	1837	AAAATTTATCAAATTTTGGCTTCAATCAAAGGGATACAGGCAACAATATATATACAAGAAG	1896
QY	2794	TGCAGAAGTTTACTAGATTTAGACATGACAGTATCAAGAGTATCAAGAGTAAAAAAT	2853
Db	1897	TGCAGAAGTTTACTAGATTTAGACATGACAGTATCAAGAGTATCAAGAGTAAAAAAT	1956
QY	2854	TAAGTGTGTGTCAAAAAGAAAGCTGTCATTTAGGAATTTGCTTTTGGGAACCCAAAGA	2913
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QY	2914	TACTGTGCTAGTGAACCAACAGCTGGAAATGGACCCCTGTTCTCGACATATTTGTATGGA	2973
Db	2017	TACTGTGCTAGTGAACCAACAGCTGGAAATGGACCCCTGTTCTCGACATATTTGTATGGA	2076
QY	2974	ATCTTTTAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCAATGATG	3033
Db	2077	ATCTTTTAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCAATGATG	2136
QY	3034	AAGCTGACATTTCTGCAGATAGGAAGCTGTGATATACAAAGGAATGCTGAANAATGTGTG	3093
Db	2137	AAGCTGACATTTCTGCAGATAGGAAGCTGTGATATACAAAGGAATGCTGAANAATGTGTG	2196
QY	3094	GTTCCTTCAATTTCTCATAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAG	3153

Db	2197	GTTCCTTCAATTTCTCATAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAG	2256
QY	3154	ACAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAAACATATACCTGGAGCTA	3213
Db	2257	ACAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAAACATATACCTGGAGCTA	2316
QY	3214	CTTTATTACAAACAGAAATGACCAACAACTTTGTGTATAGCTTTGCTTTCAAGGACATGGACA	3273
Db	2317	CTTTATTACAAACAGAAATGACCAACAACTTTGTGTATAGCTTTGCTTTCAAGGACATGGACA	2376
QY	3274	AATTTTCAGGTTTGTCTTCTGCCCTTAGACAGTCAITTCAAATTTGGGTGTCAITTTCTTATG	3333
Db	2377	AATTTTCAGGTTTGTCTTCTGCCCTTAGACAGTCAITTCAAATTTGGGTGTCAITTTCTTATG	2436
QY	3334	GTGTTTCCATGACGACTTTTGGGAAGCGTATTTTAAAGCTAGAAAGTTGAAGCAGAAATTCG	3393
Db	2437	GTGTTTCCATGACGACTTTTGGGAAGCGTATTTTAAAGCTAGAAAGTTGAAGCAGAAATTCG	2496
QY	3394	ACCAAGCAGATTTATAGTGTATTTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAT	3453
Db	2497	ACCAAGCAGATTTATAGTGTATTTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAT	2556
QY	3454	CTTTTGATGAAATGGAAACAGAGCTTACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGA	3513
Db	2557	CTTTTGATGAAATGGAAACAGAGCTTACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGA	2616
QY	3514	GCACCATGAGCCTTTGGAAACCAACAGATGTATACATATGCAAGTTCATTTCTTTACCT	3573
Db	2617	GCACCATGAGCCTTTGGAAACCAACAGATGTATACATATGCAAGTTCATTTCTTTACCT	2676
QY	3574	TGAAACGTGAAAGTAAATCAGTGAGATCAGTGTGTCTTCTGCTTTTAAATTTTTTTCACAG	3633
Db	2677	TGAAACGTGAAAGTAAATCAGTGAGATCAGTGTGTCTTCTGCTTTTAAATTTTTTTCACAG	2736
QY	3634	TTTCAGATTTTATGTTTTTGGTTTCATCTCTTTTAAATGCTGTGGTTTCCCATCAAAAC	3693
Db	2737	TTTCAGATTTTATGTTTTTGGTTTCATCTCTTTTAAATGCTGTGGTTTCCCATCAAAAC	2796
QY	3694	TTGTTTCCAGACTTATATTTTCTAAACCTGGAGACAAACCAATATATACAAACAAAGTC	3753
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Db	2857	TGCTTCTTCAAAATTTCTGCTGGTGAGAGTGTWNGTGAAGCTCAGATATCAGTGATCTTA	2916
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Db	3037	CAGCTGTTTTTCAACAGTACTATGTTTATTTTACTTATATTTAGTGAATATCATTTAGTA	3096
QY	3976	ACTTACTATCTTTATCATTTTAAATGTGACTGAAACCATCCAGATCTCGAGTACCCCATCT	4035
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QY	4096	G-AATCATTTTACTGCAATGCCACTTACTTTTGGCAATGCAAAATTCAGAGAAATCAATAG	4154
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[illegible]

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subfamily).
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VERSION
AJ275973.3 GI:22080663
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ABCA subfamily; ATP-binding cassette protein.
SOURCE
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Petry, F., Kotthaus, A. and Hirsch-Ernst, K.I.
Molecular cloning and tissue distribution of a novel ATP-binding
cassette (ABC) transporter belonging to the subfamily ABCA
Unpublished
2
Hirsch-Ernst, K.I.
Direct Submission
Submitted (02-MAR-2000) Hirsch-Ernst K.I., Department of
Toxicology, University of Goettingen, Robert-Koch-Strasse 40,
Lowery Saxony, D-37075, GERMANY
revised by [3]
3
(bases 1 to 5096)
Hirsch-Ernst, K.I.
Direct Submission
Submitted (20-NOV-2001) Hirsch-Ernst K.I., Department of
Toxicology, University of Goettingen, Robert-Koch-Strasse 40,
Lowery Saxony, D-37075, GERMANY
On Aug 1, 2002 this sequence version replaced gi:17046099.
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Query Match 77.2%; Score 5039; DB 9; Length 5096;
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Matches 5042; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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VERSION AX417824.1 GI:21522942
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS Hu, Y. and Nepomnichy, B.
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LEXICON GENETICS INC (US)
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LOCUS AX417826 4785 bp DNA linear PAT 18-JUN-2002
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ACCESSION AX417826
VERSION AX417826.1 GI:21522943
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS Hu, Y. and Nepomnichy, B.
TITLE Human transporter proteins and polynucleotides encoding the same
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LEXICON GENETICS INC (US)
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Db 181 GTGCCTAATATAGAACTCAATCTATATGGACAGTCTTCTTCTTCTTCTTCTTCTTCTTCT 240
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Db 241 TATATCTCCAGTGACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
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Db 301 CTGTATGTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
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Db 361 TCTTAAGCCGAGCAACTTTGTAGTGTGGTTTTCAGAGACCTCCATGCTCTTATGAACCTCGT 420
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QY 1491 AAATCAATGTGAGCTCTCAGTACTCGTCTCAGTCTCTCAGTCTCTCAGTCTCTCAGTCTCT 1550
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Db 481 AAATCAATGTGAGCTCTCAGTACTCGTCTCAGTCTCTCAGTCTCTCAGTCTCTCAGTCTCT 540
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QY 1551 GATGCTGCCATTTATACAGTTGAAGCAATGTTTCTCTTTGGAGAGCTGGAGTCAACT 1610
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Db 541 GATGCTGCCATTTATACAGTTGAAGCAATGTTTCTCTTTGGAGAGCTGGAGTCAACT 600
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QY 1611 AAAGCTGTTTATTAATGGAGAACTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTA 1670
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Db 2941 CCTATATAGTGAATATCATAGTAACATACTATCTTTATCAATTTAAATGTGACTGAAC 3000
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Db 3961 TTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTTGGTCCAAATGGTGTGGCCAAAGC 4020
Qy 5031 ACAATTTAATATTTCTGTTGGTATATTTGAAACCAATTTGAGCCAGGATTTTATAGGA 5090
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RESULT 11

AF491842 5347 bp mRNA linear ROD 25-FEB-2003
LOCUS Mus musculus APP-binding cassette transporter sub-family A member 5
DEFINITION (Abca5) mRNA, complete cds.
ACCESSION AF491842
VERSION AF491842.1 GI:22087247
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 5347)
AUTHORS Annino, T., Chen, Z.-Q., Shulenin, S. and Dean, M.
TITLE Evolutionary analysis of a cluster of ATP-binding cassette (ABC) genes
JOURNAL Mamm. Genome 14 (1), 7-20 (2003)
MEDLINE 22419899
PUBMED 12532264
REFERENCE 2 (bases 1 to 5347)
AUTHORS Annino, T., Chen, Z.-Q., Shulenin, S. and Dean, M.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2002) Laboratory of Genomic Diversity, National

[illegible]

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Db 1930 AAGAAATATGATGGCATTTGTCACAGATTAGATATACACTTTGATGTTTTCAGAGTAG 1989
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Db 3130 GTACTATGTTTATTTGTTTCCAGTCAATGATGAACATCATATTAGTAACTACTATCTTTATC 3189
Qy 3991 ATTTAAATGTGACTGAACCAATCCAGATCTGAGTACCCCATTTCTTTCAAGAAATTACTG 4050
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Qy 4471 TAACTTTCTTTATGGGATACAAATTTGCAACTATTTCTTCAATATGCTTTTGTATCATCA 4530
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Qy 4531 TTCCAATCTATCCACTTCTAGTTGCTGATTTCTTTTCAATAAGATTTCTTTGGAAGATG 4590
Db 3730 TTCCAATCTATCCCTCTCTGGGTTGTGTATTTCTTTTCAATAAGGTTTCTTTGGAAGATA 3789

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Db	3790	TGCCAAAAAATGGAATACCTACAAATCCCTGGGATAGACTTTTAGTTGCTGTATCATGC	3849
Qy	4651	CTTACCTGCAGTGTGTACTCTGGATTTTCTCTTACAACTACTATGAGAAAAATATGGAG	4710
Db	3850	CCTACCTGCAGTGTATAGTCTGGATTTTCTCTTACAACTACTATGAGAAAAATATATGGAG	3909
Qy	4711	GCAGATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAAAGCAAGCTTAAAAATAGGA	4770
Db	3910	GCAGATCTATAAGAAAGATCCATTTTTCAGGGCCCTTTTCAAAGGCCCAAAATAGA	3969
Qy	4771	AGCTTCCAGAAACCAACAGACAATGAGGATGAAGATGTCAAAGCTGGAAGACTAA	4830
Db	3970	AGTTTCCAGAAACCAACCCATCAATGAGGATGAAGATGAAGATGTCAAAGCTGGAAGACTGA	4029
Qy	4831	AGGTCAAAGAGCTGATGGTGTGCCAGTGTGTGAGGAGAAACCATCAATTATGGTCAGCA	4890
Db	4030	AGGTTAAAGAGCTGATGGTGTGCCAGTGTGTGAGGAGAAAGCCAGCCATTTATGGTATGCA	4089
Qy	4891	ATTTGTCATAAAGAAATATGATGACAAGAAAGATTTTCTTTTCAAGAAAAAGTAAAGAAAG	4950
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Qy	4951	TGGCAACTAAATACATCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTTGGGTC	5010
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Qy	5011	CAATGTGTCTGGCAAAAGCAATTAATTAATTTCTGGTTTGGTGATATTGAACCAACTTT	5070
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Qy	5071	CAGGCCAGTATTTTATAGGAGATTTATTTCTTCAGAGACAAGTGAAGATGATGATTTCACTGA	5130
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Qy	5131	AGTGATGGGTGTACTGTCTCAGATAAACCTTTTGTGGCCAGAGTACTACATTTGCAGGAAC	5190
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Qy	5191	ATTTTGAATTTTATGAGAGCTGTCAAAGGAATGAGTGCAGTGACATGAAGAAGTCTATAA	5250
Db	4390	ATTTTGAATTTTACGGAGCTGTGAAGAGGAATGAGTCTCTGTGTGAATGAAGGAAGTCTATCA	4449
Qy	5251	GTCCAAATAACACATGCCTTGAATTTAAAGAAACATCTTCAGAAGCTGTAAAGAAACTAC	5310
Db	4450	GTCCAAATAACAAAGGCCCTTGATTTGAAGAAACATCTTCAGAAGCTGTAAAGAAAGCTAC	4509
Qy	5311	CTGCAGGAATCAAAAGAAAGTTGTGTGTGTCTTAAGTATGCTAGGGAATCCTCAGATTA	5370
Db	4510	CTGCAGGGAATCAAGCGAAAGCTGTGTGTGTCTCAGCATGCTGGGGAACCCCTCAGGTGA	4569
Qy	5371	CTTTGTAGATGAACCATCTACAGGTATGGATCCCAAAGCCAAAACAGCACATGTGGCGAG	5430
Db	4570	CGCTGCTGGATGAGCCGTCCACAGGATGGACCCCAAGAGCCAAGCAGCAATGTGGAGAG	4629
Qy	5431	CAATTCGAACCTGCATTTTAAAAACAGAAAGCGGGCTGTATTCTTGACCACTCACTATATGG	5490
Db	4630	CTATTCGAACCTGCATTTTAAAAACAGAAAGCGGGCGGGCCCTCCTGACTACTCATTTACATGG	4689
Qy	5491	AGGAGGCAGAGGCTGTCTGTGATCCAGTGTATCATGTGTGTCTGCGCAGTTAAGATGTA	5550
Db	4690	AAGAGGCAGAGGCTGTCTGTGACAGAGGGGCCATCATGGTATCTGGCAGCTAAGATGTA	4749
Qy	5551	TCGGAAACAGTACAACATCTAAAGAGTAAATTTTGGAAAAGGCTACTTTTGGAAATTAATAT	5610
Db	4750	TTGGAAACAGTACAACATCTAAAGAGTAAATTTTGGTAAAGGCTACTTTTGGAAATTAATAT	4809
Qy	5611	TGAGGAGCTGGATAGAAAACCTAGAGTAGACCGGCTTCAAAGAGAAATTCAGTATATTTT	5670
Db	4810	TAAAGGAGCTGGATAGAAAACCTGGAAAATAGATCCGCTTCAAAGAGAAATTCATATATTTT	4869
Qy	5671	TCCCAAAATGCAAGCCGTGAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGG	5730

Db	4870	TCCCAATGCAAGCCGCAAGAGAGCTTTCTTCTATTTTGGCTTTTAAATTCAAAAG	4929
Qy	5731	AAGATGTCAGTCCCTTTTACAAATCTTTTTTAAAGCTGGAAGAAGCTAAACATGCTTTTG	5790
Db	4930	AAGATGTCAGTCTCTCTCACAATCCTTCGCTAAGTTGGAAGAAGCAAAACGCACTTTTC	4989
Qy	5791	CCATTGAAGAATATAGCTTTTCTCAAGCAACATGGAACAGAGTTTTTGTAGAACTCACTA	5850
Db	4990	CCATTGAAGAATACAGCTTTTCTCAAGCAACCTCGGAACAGGTTTTTGTAGAACTTACTA	5049
Qy	5851	AAGAACAGAGGAGGAAGATATATAGTTGTGGAACTTTAAACAGCACACTTTGGTGGGAAC	5910
Db	5050	AAGAGCAAGAGGAGGAAGATAAACAGCTGTGGGACTTTGGCCAGCACCTCTCTGTGGGAAA	5109
Qy	5911	GAACACAAGAGATAGAGTAGTATTTTGAATTTGTAT-----	5947
Db	5110	GGAAGCAGGAGGATAGTAGTATTTTGAATGTTATGCTCACCCAGCCTACCGACCTG	5169
Qy	5948	TGTTGGCTGCTTACTGGGACTTCTTCTTTTCACTTAATTTTAACTTTGGTTTAAAA	6007
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Qy	6008	AGTTTTTTATGAAATGGTAACTGGGAACCAAGACGACTTTGAAATTTTCTAAGCTC	6067
Db	5230	AGCTTATTACTTGAATAGTTA-TTAAAAAAATGAAAGCACTTTGGAAATTTCTTAAAGTC	5288
Qy	6068	CTTAATTTGAATCCTGTGGTGTGTGTTTGTCTTTTCTTTTAAATAAAACATATGTA	6123
Db	5289	CTTAATTAACACACCAATGGTTATGGTTGGATTTCTTCAATAAATTTGCGTGTATA	5344
RESULT 12			
RNO426052			
LOCUS	RNO426052	5170 bp	linear
DEFINITION	Rattus norvegicus mRNA for Abca5 protein.		
ACCESSION	AJ426052		
VERSION	AJ426052.2		
KEYWORDS	abca5 gene; ATP-binding cassette protein.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
REFERENCE	1		
AUTHORS	Petry, F., Kothaus, A. and Hirsch-Ernst, K.I.		
TITLE	Cloning of human and rat ABCA5/Abca5 and detection of a human splice variant		
JOURNAL	Biochem. Biophys. Res. Commun. 300 (2), 343-350 (2003)		
MEDLINE	22392638		
PUBMED	12504089		
REFERENCE	2 (bases 1 to 5170)		
AUTHORS	Petry, F.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-DEC-2001) Petry F., Department of Toxicology, Georg-August-University Goettingen, Robert-Koch-Strasse 40, Lower Saxony, D-37075 Goettingen, GERMANY		
REMARK	revised by author [27-AUG-2002]		
FEATURES	Location/Qualifiers		
source	1. .5170		
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Qy 2971 GGAATCTTTTAAAATACAGAAAAGCCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGG 3030
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Query Match 59.3%; Score 3868.8; DB 10; Length 4929;
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QY	1071	AAATTACTTAATAATGCAGAACCAAAAGAGTAGTCTTCAGGAAATCTTTTCCACTA	1130
DB	61	AAATTACTTAATAATGCAGACTAATAAAGTAGTCTTCAGGAAATCTTTTCCCTTA	120
QY	1131	TTTTTTTTTATTTGGTTTAATTAATTAGCATGATGCATCCAAATAGAAATAGAGAA	1190
DB	121	TTTTTCTTATTTGGCTGATATTAGTTAGCATGATGCATCCAAATAGAAATAGAGAG	180
QY	1191	GTGCTTAATAGAACTCAATCCTATGACAGAGTTTACTCTTCTTAATCTAATCTTGA	1250
DB	181	GTATCTGATATAGAGCTCAGCCCTATGACAAATTCAGCCCTTTCCAACTTATCTTGA	240
QY	1251	TATACTCCAGTGACTAATATTACAGCAGCATCATGACAGAAAGTGCTACTGATCATCTA	1310
DB	241	TACACTCCGTGACTACATTAACAGCAGCATTAATGACAGAGGTTTCTACCGATCATCTT	300
QY	1311	CCTGATGCTAATATTCTGAAGAATATACAAATGAAAGAAATGTTTAAATCAAGTCTC	1370
DB	301	CCCAAGGTTATAGTTACTGAAGAATACGCAATAGAGAAAGAACTGGTAGCCGCAAGTCTT	360
QY	1371	TCTAAGCGGACCACTTTGTAGGTGCTGTTTCCAAAGCTCCATGCTCTATGAACTCGT	1430
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QY	1431	TTTTTCTCTGATATGATTCAGATCTCTTCTATTATATGATTCAGAGCTGGCTGTTC	1490
DB	421	TTTTTCTCTGATATGATTCAGATCTCTTCTATTATATGATTCAGAGAGGCTGTTC	480
QY	1491	AAATCATGTGAGGCTGCTAGTACTGTGCTCAGGTTTCAAGTTTACAAAGCATCCATA	1550
DB	481	AAGACATGTGATGCTGCTAGTACTGTGCTTGGGTTTACAGTTCTGCGAGCATCGATA	540
QY	1551	GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAGAGGCTGGAGTCACT	1610
DB	541	GATGCTGCCATTATACAGTGAAGACCAATGTTTCTCTGTTGGAGAGGCTGGAGTCAAC	600
QY	1611	AAAGCTGTTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTA	1670
DB	601	AAAGCTGTGATCATGGAGAGGCGCTGTTGTGAGAAITGACACCTTCCCGAGGAGGTC	660
QY	1671	ATTTTAAATATACCTAGTTATAGCAATTTTCACTTTTGGATATCTTTTGGCAATTCATATC	1730
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QY	1731	GTACGAGAAAGAGAAATAAAGAAATTTTAAAGATATGGGACTTCATGATACT	1790
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DB	781	GCTTTTGGCTTCTCTGGGTTCTTCTGACGCAAGCTTGATTTTCTTATGTCCCTGCTT	840
QY	1851	ATGCGAGTCATTTGCCACAGCTTCTTTGTTATTTCTCTCAAGTAGCAGATTTGTGATATT	1910
DB	841	ATGGCTGTCAATCGCAACAGCTTCTTCGTTATTTCCCTCAGAGTAGCAGCATTTGTGATCTT	900
QY	1911	CTGCTTTTTTCTTTATAGGATATATCATCTGTATTTTTTGTCTTTAATGTCGACACTCTT	1970
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QY	1971	TTTTAAAAATCAAAACATGTGGGAATAGTTGAATTTTTTTGTACTGTGGCTTTTGGATTT	2030
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DB	1141	AATGAAGTGTCTTCAATTTTCAAAATTTGATGTCAGGCCCATATCTCTAATTTATTAATTT	1200
QY	2211	ATCATGCTCACACTTAATAGTATATCTATGCTCTTCTGGCTGTCTATCTTCTCATCAAGTC	2270
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QY	2271	ATTCCAGGGGAATTTGGCTTACGAGATCATCTTTATATATTTTCTGAAGCTTTCATATGG	2330
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DB	1321	TCAAAGAGTAAAGAAATTTATGAGAGTTTATCAGAGGGCAATGTTTAAATGGAATTTAGT	1380
QY	2391	TTTAGTGAATTTTATGAGGCTTTTCTCAGAAATTTGTAGGAAAGAGCCATATAGAAAT	2450
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DB	1441	AGTGTGTTTCAAGAGCACTACAGAAAGAGGCTGAAATTTGTGAGGCTTTGAGAAATTTG	1500
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QY	2571	AGTACATTTGATCAATTTTCTTGTGACCTCTGCCACCTTCTGATGGGTTTGCATCTATA	2630
DB	1561	AGTACATTTGATCAATTTTCTTGTGACCTCTGCCACCTTCTGATGGGTTTGCATCTATA	1620
QY	2631	TATGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAATATGATGGCAAT	2690
DB	1621	TATGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAATATGATGGCAAT	1680
QY	2691	TCTCCACAGATAGATATACATTTTGTATTTTGAAGTAAAGAAATTTTCAATTTTGT	2750
DB	1681	TCTCCACAGATAGATATACATTTTGTATTTTGAAGTAAAGAAATTTTCAATTTTGT	1740
QY	2751	GCTTCAATCAAGGNTACAGCCCAATATATACAGAGTCCGAGAGGTTTGTACTATA	2810
DB	1741	GCTTCAATCAAGGNTACAGCCCAATATATATCAAGAGTCCGAGAGGTTTGTACTATA	1800
QY	2811	GATTTAGACATGACAGTATCAAGATCAACAGCTTAAAGAAATTAAGTGGTGGTCAAAAA	2870
DB	1801	GATTTAGACATGACAGTATCAAGATCAACAGCTTAAAGAAATTAAGTGGTGGTCAAAAA	1860
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Db 3541 GGTGCTGCTGATTTCTTCAATAAAGGTTCTTGAAGAAATGTACGAAATAAATTTGTCACAC 3600
Qy 4611 TATAATCCATGGGATAGGCTTTTCAAGTGTGTTTATATGCTTTTCTGAGTGTGTAATG 4670
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Db	302	TCATCTTCCGACGCTTCTAGTTA	CTGAAGAATATACGCGAGTGAAGGAGCTGCTGGCATC	361
Qy	1364	CAGTCTCTTAAGCCGAGCACTTTG	TAGTGTGGTTTTCAAGACTCCATGTCCCTATGA	1423
Db	362	CAGTTTGTCTAAGCCGAGCACTTTG	TAGTGTGGTTTTCAAGACTCCATGTCCCTATGA	421
Qy	1424	ACTTCGTTTTTTTCTCTGATATG	ATTCAGATATCTTCTATTTATATGATTTCAAGAGCTGG	1483
Db	422	ACTGCGGTTTTTCTCTGATATG	ATTCAGATATCTTCTATTTATATGATTTCAAGAGCAGG	481
Qy	1484	CTGTTCAAAATCARTGAGGCTGCT	CAAGTCTCAAGTCTTCAAGTTTCAAGTTTCAAGC	1543
Db	482	CTGTTCAAAATCARTGAGGCTGCT	CAAGTCTCAAGTCTTCAAGTTTCAAGTTTCAAGC	541
Qy	1544	ATCCATAGATGCTGCCAATATAC	AGTTTGAAGCAATGTTTCTTTTGAAGAGGCTGGA	1603
Db	542	CTCAATAGATGCTGCCAATATAC	AGTTTGAAGCAATGTTTCTTTTGAAGAGGAGCTGGA	601
Qy	1604	GTCAACTTAAAGCTGTTATATG	GGAGAAACCTGCTGTTGTAGAAATAGATACCTTTCCCGG	1663
Db	602	GTCAACCAAGCTGTCAATCATG	GGAGAAACCTGCTGTTGTAGAAATAGATACCTTTCCACG	661
Qy	1664	AGGAGTAAATTTAATATACCT	AGTTTATAGATTTTCACTTTTGGCAAT	1723
Db	662	AGGGGTCACTCTCATCTACCT	CGTATAGCTTCTCGCCCTTCGGGTACTTTCTGGCAAT	721
Qy	1724	TCATATCGTAGCAGAAAGAA	AAAAAATTTTAAAGAAATTTTAAAGTATAGGACCTTCA	1783
Db	722	TCATATCGTAGCAGAAAGAA	AAAAAATTTTAAAGAAATTTTAAAGTATAGGACCTTCA	781
Qy	1784	TGATACCTGCTTTTGGCTTCT	CTGGTCTTCTATATACAAAGTTTAAATTTCTTATGTC	1843
Db	782	CGACACTGCTTTTGGCTTCT	CTGGTCTTCTATATACAAAGTTTAAATTTCTTATGTC	841
Qy	1844	CTTTCTTTATGGCAGTCAAT	TCGACAGCTTCTTTGTTATTTTCTCAAAAGTAGCAGCATGT	1903
Db	842	CTTTCTTTATGGCAGTCAAT	TCGACAGCTTCTTTGTTATTTTCTCAAAAGTAGCAGCATGT	901
Qy	1904	GATATTTCTGCTTTTCTTT	ATAGATATCATCTGATTTTTCGTTTAAATGCTGAC	1963
Db	902	GATTTTCTGCTTTTCTTT	ATAGATATCATCTGATTTTTCGTTTAAATGCTGAC	961
Qy	1964	ACCTCTTTTAAAAAATCA	AAAAATGSGGAATAGTTGAAATTTTCTGCTGCTGCTTT	2023
Db	962	GCCTCTTTTAAAAAATCA	AAAAATGSGGAATAGTTGAAATTTTCTGCTGCTGCTTT	1021
Qy	2024	TGGATTTTATTTGGCCTT	ATGATATCTTATAGAAAGTTTCCCAAAATCGTTAGTGGCT	2083
Db	1022	TGGCTTTTGTGGCCTT	ATGATATCTTATAGAAAGTTTCCCAAAATCGTTAGTGGCT	1081
Qy	2084	TTTCAGTCTCTTCTGCT	CACTTTTGTGATTTGGATTTGGCAGAGTCAATGATTTAGA	2143
Db	1082	CTTCAGTCTCTTCTGCT	CACTTTTGTGATTTGGATTTGGCAGAGTCAATGATTTAGA	1141
Qy	2144	AGATTTTAAATGAAGTCT	CAATTTTCAATTTTCACTGCGAGGCGCCATCTCTTAATAT	2203
Db	1142	AGATTTTAAATGAAGTCT	CAATTTTCAATTTTCACTGCGAGGCGCCATCTCTTAATAT	1201
Qy	2204	TACAAATTTATCATGCT	CACTTTTATATATATTTCTATGCTCTTCTGCTGCTCTATCTGA	2263
Db	1202	CACCTTTACCATGCT	CGCTCTGGACAGTGTGTTCTATGCTCTGCTGCTGTGTACCTTGA	1261
Qy	2264	TCAGTCAATTTCCAGGG	GAATTTGGCTTACGAGATCATCTTTATTTTCTGAAGCCTTC	2323
Db	1262	TCAGTCAATTTCCAGGG	GAATTTGGCTTACGAGATCATCTTTATTTTCTGAAGCCTTC	1321
Qy	2324	ATATTGTTCAAGAGTAA	AGAAATTTAGGAGTATCAGAGGCAATCTTAAATGAAA	2383
Db	1322	ATATTGTTCAAGAGTAA	AGAAATTTAGGAGTATCAGAGGCAATCTTAAATGAAA	1381
Qy	2384	TATTAGTTTTAGTGAA	ATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAGCCAT	2443

Db	1382	TATTAGTCTCAATGAAATTT	TGTGAGCCCGTTTTCTTCAGAATTTATAGGAAAGAGCTAT	1441
Qy	2444	AGCAATTTAGTGTGATTT	CAGAAGCATACAGAAAGAGGGTGAATACTGTGAGGCTTTGAG	2503
Db	1442	AGCAATTTAGTGTGATTT	CAGAAGCATACAGAAAGAGGGTGAATACTGTGAGGCTTTGAG	1501
Qy	2504	AAATTTGTCTAATTTG	CATATATGAGGGTCTGATTTACTGCTTACTTTGGCCACAGTGAAC	2563
Db	1502	AAATTTGTCTGTTTG	CATCTATGAGGCTCTATGAGGCGCAGATTTACTGCTCTGCTGGCCACAGTGAAC	1561
Qy	2564	AGAAAGAGTACATTTG	ATGATGAAATTTCTTTGTGGAATCTGCTCCACCTTCTGATGGGTTTGC	2623
Db	1562	AGAAAGAGTACATTTG	ATGATGAAATTTCTTTGTGGAATCTGCTCCACCTTCTGATGGGTTTGC	1621
Qy	2624	ATCTATATATGGA	CACAGAGTCTCAGAAATAGATGAAATGTTTGAACGAGAAATATGAT	2683
Db	1622	TTCTATATATGGA	CACAGAGTCTCAGAAATAGATGAAATGTTTGAACGAGAAATATGAT	1681
Qy	2684	TGGCATTTGTCCA	CAGATTAGATATACATTTTGTATGTTTGTACAGTGAAGAAATTTATC	2743
Db	1682	TGGCATTTGTCCA	CAGATTAGATATACATTTTGTATGTTTGTACAGTGAAGAAATTTATC	1741
Qy	2744	AATTTTGGCTTCAAT	CAAAAGGGATACAGCCAAATATATAAACAAGAGTGCAGAAAGT	2803
Db	1742	AATTTTGGCTTCAAT	CAAAAGGGATACAGCCAAATATATAAACAAGAGTGCAGAAAGT	1801
Qy	2804	TTTACTAGATTTAG	CATGAGATCAATCAAGATAACCAAGCTTAAATAATTAAGTGTG	2863
Db	1802	TTTACTAGATTTAG	CATGAGATCAATCAAGATAACCAAGCTTAAATAATTAAGTGTG	1861
Qy	2864	TCAAAAAGAAAGCT	GTCAATTTAGGAATTTGCTTTTGGGAACCCCAAGATATCTGCTGCT	2923
Db	1862	CAAAAAGAAAGCT	GTCAATTTAGGAATTTGCTTTTGGGAATTTGGAATCTCTCTGCT	1921
Qy	2924	AGATGAACCAAC	AGCTGGAATGGAACCCCTGTTCTCGACATATTTGATGGAATCTTTTAA	2983
Db	1922	AGATGAACCAAC	AGCTGGAATGGAACCCCTGTTCTCGACATATTTGATGGAATCTTTTAA	1981
Qy	2984	ATACAGAAAGCC	CAATCGGCTGACAGTGTTCAGTACTCATTTTCATGATGAAGTGCAT	3043
Db	1982	GTACAGAAAGGCT	TAACCGAGTGCAGTCTTCAGCACTCATCTTCATGATGAGGCGGACAT	2041
Qy	3044	TCCTTGAGATAG	GAAGCTGTGATATCAAGAGAAATGCTGAAATGTTGTTCTTCAAT	3103
Db	2042	TCCTTGAGATAG	GAAGCTGTGATATCAAGAGAAATGCTGAAATGTTGTTCTTCAAT	2101
Qy	3104	GTTTCTCTCAAA	AGTAAATGSGGGATCGGCTACCGCTGAGCATGTACATAGACAAATTTG	3163
Db	2102	TTTTCTCTGAAA	AGTAAATGSGGGATCGGCTACCGCTGAGCATGTATATAGACAGGTA	2161
Qy	3164	TGCCACAGATCT	CTTTCTTCTTCTGTTTAAACAAATATACCTGGAGCTACTTTTATACA	3223
Db	2162	TGCCACAGATCT	CTCTCGTCTGTTTAAACAAATATACCTGGAGCTACTTTTATACA	2221
Qy	3224	ACAGAAATGACC	AAACAACTTTGATAGTTCCTTTCAAGGACATGACAAATTTTTCAGG	3283
Db	2222	GCAGAAATGACC	AAACAACTTTGATAGTTCCTTTCAAGGACATGACAAATTTTTCAGG	2281
Qy	3284	TTTGTGTTTCT	CGCTTACAGATCATTTCAAAATTTGGGTGTCATTTCTTATGGTGTTCAT	3343
Db	2282	CTTGTGTTTCT	CGCTTACAGATCATTTCAAAATTTGGGTGTCATTTCTTATGGTGTTCAT	2341
Qy	3344	GACGACTTTGGA	AGAGCTATTTTAAAGCTAGAGTTGAAGAGAAATTTGACCAAGCAGA	3403
Db	2342	GACGACTTTGGA	AGAGCTATTTTAAAGCTAGAGTTGAAGAGAAATTTGACCAAGCAGA	2401
Qy	3404	TTATAGTGTATTT	TACTCAGAGCTGAGGAGGAAATGGAATTTCAAAATCTTTTGTATGA	3463
Db	2402	TTATAGTGTATTT	TACTCAGAGCTGAGGAGGAAATGGAATTTCAAAATCTTTTGTATGA	2461
Qy	3464	AATGGAACAGAG	CTTACTTTCTGAAAACCAAGGCTTCTCTAGTGTGAGCCATGAG	3523

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2642 TAGTTTTTGGTTCATCACTCTTTTAAATAGCTGTGGTTCACATCAAACTGTGTCAGA 2701 Db
3704 CTTATATTTTCTAAACCTCGAGACCAACACATAAATAAACAACAGTCTGCTCTTCA 3763 Qy
2702 CTTGTATTTTCTAAACCTCGAGATAAACCTCATAAATAAACAACAGCCTGCTGCTTCA 2761 Db
3764 AAATTTCTGCT-----GACTCAGATATCAGTGATCTTATTAGCTTTTCA 3807 Qy
2762 AAATTTCTAGTGGTGAGAGCGTGAAGATTCAGATATCAATGATCTTATTGACTTTTCA 2821 Db
3808 CAAGCCAGAACATAATCGTGACGATGAATTAATGACGTAGTATCGTGCTCCCC 3867 Qy
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4382 TCACACTGTGGATGAGCGCTCTACAGGTATGGAACCCAGAGCCCAACAGCAATGTTGGC 4441 Db
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Qy	5668	TTTTCCCAATGCAAGCGTCAGAGAAAGTTTTCTTCTATTTGGCTTATAAAATTCCTA	5727
Db	4682	TTTTCCCAATGCAAGCGTCAGAGAAAGTTTTCTTCTATTTGGCTTATAAAATTCCTA	4741
Qy	5728	AGGAAGATGTTCAAGTCCCTTTTCAAACTTTTTTTAGCTGGAGAGCTAAACATGCTT	5787
Db	4742	AAGAAGATGTTCAAGTCCCTTTTCAAACTTTTTTTAGCTGGAGAGCTAAACATGCTT	4801
Qy	5788	TTGCCATTGAAGAAATAGAGCTTTTCTCAAGCAACATTTGGAACAGCTTTTGTAGAACTCA	5847
Db	4802	TTGCCATTGAAGAAATAGAGCTTTTCTCAAGCAACCTTGGAAACAGCTTTTGTAGAACTCA	4861
Qy	5848	CTAAGAACAGAGGAGAGATATAGTTGTGGAACCTTTAAACAGACACATTTGGTGGG	5907
Db	4862	CTAAGAGCAGGAGGAGAGATATAGTTGTGGAACCTTTAAACAGACACATTTGGTGGG	4921
Qy	5908	AACGAACACAGAGATAGAGTAG	5931
Db	4922	AAAGAAGCAGGAGAGAGTAG	4945
RESULT 15			
AK094416			
LOCUS	AK094416	3347 bp	linear
DEFINITION	Homo sapiens cDNA FLJ37097 fis, clone BRACE2018847, moderately similar to ATP-binding cassette, sub-family A member 8.		PRI 15-JUL-2002
ACCESSION	AK094416		
VERSION	AK094416.1	GI:21753472	
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M., Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamaehita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.		
TITLE	NEDO human cDNA sequencing project		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3347)		
AUTHORS	Isogai, T. and Yamamoto, J.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan		
COMMENT	(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.		
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	/tissue_type="cerebellum"		
	/clone_lib="BRACE2"		
	/note="cloning vector: pME18SPL3"		
BASE COUNT	1049 a 551 c 643 g 1104 t		
ORIGIN			
Query Match	49.9%;	Score 3258.2;	DB 9; Length 3347;
Best Local Similarity	98.5%;	Pred. No. 0;	
Matches 3327;	Conservative	0; Mismatches	4; Indels 47; Gaps 2;

Qy	2999	TCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGCACATTTCTTCAGATAGGAA	3058
Db	1	TCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGCACATTTCTTCAGATAGGAA	60
Qy	3059	AGCTGTGATATACAGAGGAATGCTGAATGTGTGGTCTTCAATGTTCCTCAAAAGTAA	3118
Db	61	AGCTGTGATATACAGAGGAATGCTGAATGTGTGGTCTTCAATGTTCCTCAAAAGTAA	120
Qy	3119	ATGGGGGATCGGCTACCGCTGAGCATGTATAGACAAATATTTGTGCCACAGAACTCTCT	3178
Db	121	ATGGGGGATCGGCTACCGCTGAGCATGTATAGACAAATATTTGTGCCACAGAACTCTCT	180
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Db	181	TTCTTTCACCTGTTTAAACCAACATATACCTGGAGCTACTTTATTAACAACAGAACTCAACA	240
Qy	3239	ACTTGTGTATAGCTTGGCTTTCAAGGACATGGACAAATTTTTCAGTTTGTGGTCTCGCCT	3298
Db	241	ACTTGTGTATAGCTTGGCTTTCAAGGACATGGACAAATTTTTCAGTTTGTGGTCTCGCCT	300
Qy	3299	AGACAGTCAATCAAAATTTGGGTGCTCATTTCTTATGGTGTTCATGACGACTTTTGGGAAGA	3358
Db	301	AGACAGTCAATCAAAATTTGGGTGCTCATTTCTTATGGTGTTCATGACGACTTTTGGGAAGA	360
Qy	3359	CGTATTTTAAAGCTAGAGTTGAAGCAGAAATTTGACCAAGCAGATTTATAGTGTATTTAC	3418
Db	361	CGTATTTTAAAGCTAGAGTTGAAGCAGAAATTTGACCAAGCAGATTTATAGTGTATTTAC	420
Qy	3419	TCAGAGCCACTCGGAGGAATGGAATCAAAATCTTTTGTAGTGAATGGAACAGAGCTT	3478
Db	421	TCAGAGCCACTCGGAGGAATGGAATCAAAATCTTTTGTAGTGAATGGAACAGAGCTT	480
Qy	3479	ACTTATTTCTTCTGAACCAAGGCTCTCTAGTCAGCACCACCTGCTTTTGGAAACAACA	3538
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Qy	3539	GATGTATACAAATGCAAGGTTTCATTTCTTACCTTGAACAGTGAAAGTAAATCAGTGAG	3598
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Qy	3599	ATCAGTGTGCTCTGCTCTTTAAATTTTTCACAGTTCAGATTTTATAGTTTGGTTCA	3658
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Qy	3774	-----GACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCAGAAACATAA	3822
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Qy	3823	TGCTGAGCATGATTAATGACAGTACTATGTATCGGTGGCTCCCATAGTCGGCTTTAA	3882
Db	841	TGCTGAGCATGATTAATGACAGTACTATGTATCGGTGGCTCCCATAGTCGGCTTTAA	900
Qy	3883	ATGTGATGATTCAGAAAAGGACTATGTTTTTCAGCTGTTTTTCAACAGTACTATGTTTT	3942
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Qy	3943	ATTCTTTTACCTATATTAGTGAATATCATTTAGTAAGTAACTACTATCTTTTATCAATTA	4002
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DB |||||
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DB |||||
DB 1171 -AGGCTTTTGGCCATCTGCATATTTGGATTTGGCAAGCTGTTGTTGATATCCCTTATTTT 1229
QY 4243 TTATCATTTCTATTTTATGCTAGGAAGCTTACTGCGCATTTCAATTTCAATATGATATATTTT 4302
DB |||||
DB 1230 TTATCATTTCTATTTTATGCTAGGAAGCTTACTGCGCATTTCAATTTCAATATGATATATTTT 1289
QY 4303 ATACTGTAAAGTTCTTGTCTGTGGTTTTTGGCTTATTTGGTTATGTTTCCATCAAGTTATTC 4362
DB |||||
DB 1290 ATACTGTAAAGTTCTTGTCTGTGGTTTTTGGCTTATTTGGTTATGTTTCCATCAAGTTATTC 1349
QY 4363 TGTTCACCTTATATGCTTTCTTTCACCTTTAAGAAAATTTTAAATACCAAGAAATTTTGGT 4422
DB |||||
DB 1350 TGTTCACCTTATATGCTTTCTTTCACCTTTAAGAAAATTTTAAATACCAAGAAATTTTGGT 1409
QY 4423 CATTTATCTATCTGTGGCAGCTTGNCTTGTATTTGCAATCACTGAAATAAATCTTCTTTA 4482
DB |||||
DB 1410 CATTTATCTATCTGTGGCAGCTTGGCTTGTATTTGCAATCACTGAAATAAATCTTCTTTA 1469
QY 4483 TGGGATACACAATTTGCAATATTTCTTCAATATGCTTTTGTATCATCATTTCCAATCTATC 4542
DB |||||
DB 1470 TGGGATACACAATTTGCAATATTTCTTCAATATGCTTTTGTATCATCATTTCCAATCTATC 1529
QY 4543 CACTTCTAGTGTGCTGATTTCTTTTCAATAAGATTTCTTGGAGAATGTACGAAAAATG 4602
DB |||||
DB 1530 CACTTCTAGTGTGCTGATTTCTTTTCAATAAATTTCTTGGAGAATGTACGAAAAATG 1589
QY 4603 TGGACACCTATATPCCATGGATAGGCTTTTCACTAGCTGTTATATCGCTTACTCTGAGT 4662
DB |||||
DB 1590 TGGACACCTATATPCCATGGATAGGCTTTTCACTAGCTGTTATATCGCTTACTCTGAGT 1649
QY 4663 GTGTACTGTGGATTTTCTCTTCAATATCTATGAGAAAAATATGGAGGCGAGATCAATAA 4722
DB |||||
DB 1650 GTGTACTGTGGATTTTCTCTTCAATATCTATGAGAAAAATATGGAGGCGAGATCAATAA 1709
QY 4723 GAAAAATGCTTTTTCAGAAAATTTTCAAGAACTTCAAGAACTTAAATATGGAAGCTTCCAGAC 4782
DB |||||
DB 1710 GAAAAATGCTTTTTCAGAAAATTTTCAAGAACTTCAAGAACTTAAATATGGAAGCTTCCAGAC 1769
QY 4783 CACCAGAAATGAGGATGAAGATGAAGATGTTCAAGAACTTAAAGCTTAAAGCTTAAAGAGC 4842
DB |||||
DB 1770 CACCAGAAATGAGGATGAAGATGAAGATGTTCAAGAACTTAAAGCTTAAAGCTTAAAGAGC 1829
QY 4843 TGATGGGTGCGCAGTGTGTGAGGAGAAACCATTCATTTAGTGTGAGCAATTTGCAATAAG 4902
DB |||||
DB 1830 TGATGGGTGCGCAGTGTGTGAGGAGAAACCATTCATTTAGTGTGAGCAATTTGCAATAAG 1889
QY 4903 AATATGATGCAAGAAAGATTTTCTTTCAGAAAGATTAAGAAAGTGGGCACTTAAT 4962
DB |||||
DB 1890 AATATGATGCAAGAAAGATTTTCTTTCAGAAAGATTAAGAAAGTGGGCACTTAAT 1949
QY 4963 ACATCTCTTTCTGTGCAAAAAAGGAGAGATCTTGGACATTTTGGGTCCAAATGTTGCTG 5022
DB |||||
DB 1950 ACATCTCTTTCTGTGCAAAAAAGGAGAGATCTTGGACATTTTGGGTCCAAATGTTGCTG 2009
QY 5023 GCAAAAGCACAATTTATTAATTTCTGTTGTTGATATTTGAACCAACTTTCAGGCGCAGTAT 5082
DB |||||
DB 2010 GCAAAAGCACAATTTATTAATTTCTGTTGTTGATATTTGAACCAACTTTCAGGCGCAGTAT 2069
QY 5083 TTTTAGAGATATTTCTTCAGAGCAAGATGAGATGATTTCACTGAACTGTATGGTT 5142
DB |||||
DB 2070 TTTTAGAGATATTTCTTCAGAGCAAGATGAGATGATTTCACTGAACTGTATGGTT 2129
QY 5143 ACTGTCTCAGATAAACCCCTTTTGTGGCCAGATACCTACATTTGCAGGAACATTTTGAATTT 5202

DB 2130 ACTGTCTCAGATAAACCCCTTTTGTGGCAGATCTACATTTGCAGGAACATTTTGAATTT 2189
QY 5203 ATGAGAGCTGTCAAAGGAATAGTGCAGATGACATGAAAGAAAGTCAATAAGTGCATAAACAC 5262
DB |||||
DB 2190 ATGAGAGCTGTCAAAGGAATAGTGCAGATGACATGAAAGAAAGTCAATAAGTGCATAAACAC 2249
QY 5263 ATGCACTTGTATTTAAAGAACATCTTTCAGAGACATGTTAAAGAACTACCTCGAGGAATCA 5322
DB |||||
DB 2250 ATGCACTTGTATTTAAAGAACATCTTTCAGAGACATGTTAAAGAACTACCTCGAGGAATCA 2309
QY 5323 AACGAAAGTGTGTTTCTCTTAAGTATGCTTAGGAATCTCAGATTTCTAGTAGTG 5382
DB |||||
DB 2310 AACGAAAGTGTGTTTCTCTTAAGTATGCTTAGGAATCTCAGATTTCTAGTAGTG 2369
QY 5383 AACCATCTACAGGTATGATCCCAAGCCAAACAGCACATGTTGGCGAGCAATTCGAACTG 5442
DB |||||
DB 2370 AACCATCTACAGGTATGATCCCAAGCCAAACAGCACATGTTGGCGAGCAATTCGAACTG 2429
QY 5443 CATTTAAAAACAAGAAAGCGGCTGCTATTTCTGACCACTCAGTATATGAGGAGGCGAGAG 5502
DB |||||
DB 2430 CATTTAAAAACAAGAAAGCGGCTGCTATTTCTGACCACTCAGTATATGAGGAGGCGAGAG 2489
QY 5503 CTGCTCTGATCGAGTAGCTATCATGTTCTGCGCAGTTAAGATGTTAGGAAACAGTAC 5562
DB |||||
DB 2490 CTGCTCTGATCGAGTAGCTATCATGTTCTGCGCAGTTAAGATGTTAGGAAACAGTAC 2549
QY 5563 RACATCTAAGAGTAAATTTTGGAAAGGCTACTTTTGGAAATTAATTTGAAGGACTCGA 5622
DB |||||
DB 2550 AACATCTAAGAGTAAATTTTGGAAAGGCTACTTTTGGAAATTAATTTGAAGGACTCGA 2609
QY 5623 TAGAAAACTAGAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCCCAATGCAA 5682
DB |||||
DB 2610 TAGAAAACTAGAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCCCAATGCAA 2669
QY 5683 GCCGTGAGGAAAGTTTCTTCTATTTTGGCTTATAAATTCCTAAGGAAGATGTTCACT 5742
DB |||||
DB 2670 GCCGTGAGGAAAGTTTCTTCTATTTTGGCTTATAAATTCCTAAGGAAGATGTTCACT 2729
QY 5743 CCCTTTCACATCTTTTCTTAAAGCTGGAAGAGCTTAAACATGCTTTTCCCATTTGAAGAT 5802
DB |||||
DB 2730 CCCTTTCACATCTTTTCTTAAAGCTGGAAGAGCTTAAACATGCTTTTCCCATTTGAAGAT 2789
QY 5803 ATAGCTTTTCTCAAGCAACATTTGGAACAGAGTTTGTAGAACTCACTAAAGAACAGAGG 5862
DB |||||
DB 2790 ATAGCTTTTCTCAAGCAACATTTGGAACAGAGTTTGTAGAACTCACTAAAGAACAGAGG 2849
QY 5863 AGGAAGATAATAGTTTGTGAACTTTTAAACAGCACACTTTGTTGGGAAACGAAACAGAGAG 5922
DB |||||
DB 2850 AGGAAGATAATAGTTTGTGAACTTTTAAACAGCACACTTTGTTGGGAAACGAAACAGAGAG 2909
QY 5923 ATAGAGTAGTATTTTGAATTTTGTATTTGCTGCTTCTTACCTGGAATCTTTCTTTTTC 5982
DB |||||
DB 2910 ATAGAGTAGTATTTTGAATTTTGTATTTGCTGCTTCTTACCTGGAATCTTTCTTTTTC 2969
QY 5983 ACTTAATTTTAACTTTTGGTTTAAAGTTTAAATTTTGAATGCTTAACTGGAACCAAGA 6042
DB |||||
DB 2970 ACTTAATTTTAACTTTTGGTTTAAAGTTTAAATTTTGAATGCTTAACTGGAACCAAGA 3029
QY 6043 ACGCACTTGAAATTTTCTAAGCTCTTAATTTGAATGCTGTTGGTGTGTTTGTCTTT 6102
DB |||||
DB 3030 ACGCACTTGAAATTTTCTAAGCTCTTAATTTGAATGCTGTTGGTGTGTTTGTCTTT 3089
QY 6103 TCTTTTAAATAAGCTATGATTAATAAGTGAAGCTGCAATTTGTTTGAAGTATATG 6162
DB |||||
DB 3090 TCTTTTAAATAAGCTATGATTAATAAGTGAAGCTGCAATTTGTTTGAAGTATATG 3149
QY 6163 AACTATATAGTTTGTATGTCATCTTTTCCCAATTCAGAAACAGTCTTCTGAAATTTG 6222
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DB 3150 AACTATATAGTTTGTATGTCATCTTTTCCCAATTCAGAAACAGTCTTCTGAAATTTG 3209
QY 6223 ATTTAAGGAATTTGTAATAGAAATGTTTATTTTAAAGTTATCTTTAAAGTTATGCAATC 6282

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Qy	6283	TTCTTAAATAAGTACGTAATGTTCCCAATCTAAATATAAAAACTAATACATAACTAATGCGAT	6342
Db	3270	TTCTTAAATAAGTACGTAATGTTCCCAATCTAATATAAAAACTAATACATAACTAATGCGAT	3329
Qy	6343	AGAAAAGATACATAAAGC	6360
Db	3330	AGAAAAGATACATAAAGC	3347

Search completed: January 31, 2004, 00:03:03
Job time : 15262 secs

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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 19:12:41 ; Search time 282 Seconds
(without alignments)
10212.854 Million cell updates/sec

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Perfect score: 6525
Sequence: 1 aaatgtgatattttctt.....ttgatcataataagtgaat 6525

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159.2	2.4	5894	3	US-08-665-259-24
2	159.2	2.4	5894	3	US-08-762-500-24
3	159.2	2.4	6525	3	US-08-762-500-74
4	103.4	1.6	1064	4	US-08-858-207A-88
5	92.2	1.4	5625	4	US-08-961-527-1
6	80.6	1.2	795	4	US-08-961-527-264
7	77.2	1.2	696	4	US-09-134-001C-987
8	75.8	1.2	1026	4	US-09-134-001C-1205
9	75	1.1	774	4	US-09-107-532A-412
10	74.6	1.1	1664976	4	US-08-916-421B-1
11	72.2	1.1	768	4	US-09-107-532A-1681
12	71	1.1	1664976	4	US-08-916-421B-1
13	69.8	1.1	990	4	US-09-107-532A-1190
14	69.2	1.1	969	4	US-09-107-532A-1008
15	68.4	1.0	19124	2	US-08-487-826B-13
16	65.8	1.0	4848	4	US-08-961-527-185
17	65.8	1.0	5717	4	US-08-961-527-102
18	65	1.0	1770	4	US-09-328-352-3466
19	64.6	1.0	3144	4	US-08-961-527-224
20	64.6	1.0	6273	4	US-08-961-527-21
21	63.2	1.0	7218	1	US-08-232-463-14
22	63	1.0	14672	4	US-08-961-527-111
23	62.4	1.0	580073	4	US-08-545-528D-1
24	62	1.0	1230025	4	US-09-198-452A-1
25	61.4	0.9	1797	4	US-09-107-532A-2383
26	59.6	0.9	858	4	US-09-107-532A-2722
27	59.2	0.9	678	4	US-09-134-001C-378

28	58.8	0.9	15567	4	US-09-627-376-3	Sequence 3, Appli
29	58.4	0.9	5852	1	US-07-867-106-2	Sequence 2, Appli
30	57.6	0.9	1038	4	US-09-107-532A-195	Sequence 195, App
31	57.6	0.9	6846	4	US-08-961-527-198	Sequence 198, App
32	57.2	0.9	690	4	US-09-134-001C-1276	Sequence 1276, Ap
33	57	0.9	876	4	US-09-107-532A-551	Sequence 551, App
34	56.2	0.9	873	4	US-09-134-001C-436	Sequence 436, App
35	56.2	0.9	1404	4	US-09-134-001C-615	Sequence 615, App
36	56	0.9	618	4	US-09-107-532A-1929	Sequence 1929, Ap
37	56	0.9	771	4	US-09-107-532A-554	Sequence 554, App
38	55.8	0.9	813	4	US-09-134-001C-2724	Sequence 2724, Ap
39	55.2	0.8	783	4	US-09-107-532A-1996	Sequence 1996, Ap
40	54.8	0.8	933	4	US-09-134-001C-2350	Sequence 2350, Ap
41	54	0.8	765	1	US-08-232-463-14	Sequence 14, Appl
42	54	0.8	7218	1	US-08-232-463-14	Sequence 14, Appl
43	52.8	0.8	747	4	US-09-134-001C-894	Sequence 894, App
44	52.2	0.8	948	4	US-09-328-352-262	Sequence 262, App
45	51.8	0.8	1014	4	US-09-134-001C-2713	Sequence 2713, Ap

ALIGNMENTS

RESULT 1
US-08-665-259-24
; Sequence 24, Application US/08665259
; Patent No. 6028173
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES, AND USING SAME
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES, AND USING SAME
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IGS-9.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..5053
US-08-665-259-24

Query Match 2.4%; Score 159.2; DB 3; Length 5894;

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 264:

SEQUENCE CHARACTERISTICS:

LENGTH: 795 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-961-527-264

Query Match 1.2%; Score 80.6; DB 4; Length 795;

Best Local Similarity 48.3%; Pred. No. 3.6e-09;

Matches 320; Conservative 0; Mismatches 334; Indels 9; Gaps 3;

QY 4945 AGAAGTGGCACTAATATCATCTCTTCTGTGTGAAAAAGAGAGATCTTAGGACTAT 5004

Db 3 ATAAAGAGGCTTGTAGTAATCTCAATTTGCAGATTGAAATGGAGAGATTATGGGCTGA 62

QY 5005 TGGTCCAAATGCTGCGCAAAAGCACAAATTATTAATTTCTGTGTTGGTGATTTGAAC 5064

Db 63 TTGGTCATAATGGGCTGGAAATTCGACCACTATAAATCCCTAGTCAGTATCATTTTAC 122

QY 5065 CAACCTCAGGCCAGGTATTTTATAGGAGATTATTTCTTCAGAGACAAGTAGATGATT 5124

Db 123 CCAGCAGTGTCTATTTTGTAGACGCTCAGGAGTATCGGAAATCGCTCGCTATTA 182

QY 5125 CACTGAAGTGTGGTTACTGTCTCAGATAAACCCCTTTGTGCGCAGATACACTATGC 5184

Db 183 AACGAAAG---ATTGGCTAGCTAGCAGACTCGCTGACTATTTTACCGTTAACGCCCA 239

QY 5185 AGGAACATTTTGAATTTATTTGGAGCTGTCAAAGGAATGAGTCAAGTGCATCAAAAGAG 5244

Db 240 ATGAATTTTGGGAATTGATCGCTCATCTCTATGATCTGATAGTATCTGACTTGGAGCTA 299

QY 5245 TCATAAGTCGAATAACACATCGCACTTGATTTAAAGAAACATCTTCAGAAGACTGTAAAGA 5304

Db 300 GTCTAGCTAGCTATTGAACGTTTGTGATTTTCTGTAATCGCTATCAGGTTATTGAA 359

QY 5305 AACTACCTGAGGAATCAAAAGAAAGTTGTTTGTCTCTAATGATGCTAGGGAATCCTC 5364

Db 360 CTCTTTCTCAGGAAATCGTCAAGAACTCTTTGTCTATCGGAGCACTCTTGTCTGATCCCG 419

QY 5365 AGATTACTTTGCTAGTAGTACCATCTACAGTATGATCCCAAGCCAAACACACATGT 5424

Db 420 ATATTTGGGCTTGGATGAACCTTTGACTGGTTGGATCCCAAGCTGCCCTTTGA---TT 476

QY 5425 GCGAGCAATTCGAATCTGCAATTTAAACACAGAAGCGGGCTGCTATTTCTGACCACTCACT 5484

Db 477 TGAACAGATGATCAAGAACATCGACAAAGGGAAGACAGTCTGTTTCACTCATG 536

QY 5485 ATATGAGAGGCGAGAGGCTGTCTGTGATCAGTAGCTATCATCTGTGCTGCGGCACTTAA 5544

Db 537 TCCTAGAGGTGGCAGACAAAGTCTGTGATCGGATTTGCCATTTTGAAGAAAGGGGCATTTGA 536

QY 5545 GATCTATCGAACAGTACACATCTAAGAGTAAATTTGGAAAGGCTACTTTTTCGAA 5604

Db 597 TTTATTTGGTGTAGTAGGACTT---GAGAAAGATTACCCAGACCACTCTTTGAA 653

QY 5605 TTA 5607

Db 654 GTA 656

RESULT 7

US-09-134-001C-987

; Sequence 987, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 987

; LENGTH: 696

; TYPE: DNA

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-987

Query Match 1.2%; Score 77.2; DB 4; Length 696;

Best Local Similarity 48.0%; Pred. No. 2e-08;

Matches 285; Conservative 0; Mismatches 303; Indels 6; Gaps 2;

QY 4936 GAAAAGTAAAGAAAGTGGCACTAAATACATCTCTTCTGTGTGAAAAAGAGAGATCT 4995

Db 50 GATATGGAATAAAACCTGTAATTAAGATTGAAATTTGAATTAGAAAAAGCTGAAATTTG 109

QY 4996 TAGGACTATTGGTCCAAATGCTGCGCAAAAGCACAAATTATTAATTTCTGTTGGTG 5055

Db 110 TAGGTTAATAGGCTTAATGCTGCGGAAAGTACTACAATTAACATATGCTAGGAT 169

QY 5056 ATATTGAACCAACTTCAGGCCAGGTATTTTATAGGAGATTATTTCTTCAGAGACAAGTGAAG 5115

Db 170 TGAATTANTCCAATGGAAGCAAAATTATCAATTTCAATATTAATAATTAATGAATATTG 229

QY 5116 ATGATGATTCACTGAAGTGTATGGGTACTGTCTCAGATAAACCCCTTTGTGGCCAGATA 5175

Db 230 AAAATTATAGAAAGAGT---TATCTTATATACCTGGAATCACCAGTCACTATGATGAAC 286

QY 5176 CTACATTCGAGCAACATTTTGAATTTATGGAGCTGTCAAAGGAATGAGTCAAGTGACA 5235

Db 287 TAACTTTAGAGGAGCACATTTGAAATGACGGCGATGCTTATCAATTAAGTAGAGAGAGG 346

QY 5236 TGAAGAAGTCTATAAGTCCGAATAACACATGCACTTTGATTTAAAGAAACATCTTCAGAAGA 5295

Db 347 TTATCGGTAGACTAAACCAATTACTTAAAGTTTTTAGATTAGAAATGAACTTAAAGTAT 406

QY 5296 CTGTAAGAAACTACTCTCGAGGAATCAAAAGAAAGTTGTTTGTCTCTAAAGTATGCTAG 5355

Db 407 TTCCAAGTCATTTTCTAAAGGGATGAAACAAAAAGTGATGATTATTTGTGCATTTATAG 466

QY 5356 GGAATCCTCAGATTACTTTGTGTAGTAGAACCATCTACAGTATGNTCCCAAGCCCAAC 5415

Db 467 TTGATCCAGAAATTATATATTATTTGACGAACCTTTCTCGGTTTAGATCTTTGGGATAC 526

QY 5416 AGCACATGTGGCGAGCAATTCGAACCTGCAATTTAAAAACAGAAAGCGGGCTGCTATTCTGA 5475

Db 527 AGTCTATGTAGATTATATGTTA---GAAAAAGAAATGAAATCGAACAGTATTATATGA 583

QY 5476 CCACCTCACTATATGAGGAGGCGAGGCTGTCTGTGATGAGTAGCTATCATGCG 5529

Db 584 GTACACATATTTTGGCTACAGCCGAAAGGTATTTGTGATAGATTATTTATTATTAG 637

RESULT 8

US-09-134-001C-1205

; Sequence 1205, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1205
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1205

Query Match 1.2%; Score 75.8; DB 4; Length 1026;
Best Local Similarity 47.8%; Pred. No. 4.9e-08;
Matches 255; Conservative 0; Mismatches 272; Indels 6; Gaps 1;

QY 2456 TATTCAGACATACAGAAAGAGGTGAAATGTGGAGCTTTGAGAAATTTGTCATT 2515
DB 18 TGTAAACAAAGTTTTCGCAAAAAGAGAACTATTCAAGCTTTGAAAAATGTATCAAT 77

QY 2516 TGACATATATGAGGTCAGATTACTGCTTACTTTGGCCACAGTGGACAGAAAGAGTAC 2575
DB 78 TAGATTGACCAACATGATATTTTGGTGTATTGGTTATGTAGTGTCTGGTAAAGTAC 137

QY 2576 ATTGATGAATATCTTTGTGGACTCTGCCACCTTCTGTATGGGTTTGCATCTATATATGG 2635
DB 138 ATTAGTTCCGTTAGTCAATCACTTGACAGCATATCAGATGTCAAGTATTGTTGATGG 197

QY 2636 ACACAGATC-----TCAGAAATAGATGAAATGTTTGAAGCAAGAAATGATGGCAT 2689
DB 198 TCATGAGATTGATACATATAAAGAAAAAGATTTACGTGATATTAAAAAAAGATATCGGTAT 257

QY 2690 TTGTCCACAGTTAGATATACATTTTGATGTTTTCACAGTAGAAGAAATTTATCAATTT 2749
DB 258 GATCTTTCAACATTTTCTTAATCTTAAATCAGTCTTATAAAATGTTGCAATGCC 317

QY 2750 GGCTTCAATCAAGGGGATACCCAGCAACATATAATACAAAGAGTGCAGAGGTTTACT 2809
DB 318 ACTTATTTAAGTAAGCAAAATAGAAAGAAATTAAGGAAGAAAGTTGACCAATGTTAGA 377

QY 2810 AGATTAGACATGACACTATCAAGATAACCAAGCTTAAATAATTAAGTGGTGTCAAAA 2869
DB 378 ATTGTGGGGCTTCTGATATAAAGATCAATTTCCAGATGAATATATCAGGTGGACAAA 437

QY 2870 AAGAACTGTCTATGAGATTTGCTTCTTGGGAACCAAGATCTGCTGCTAGATGA 2929
DB 438 ACAACGTGTTGCCATCCAGAGCATTAGTAACGCATCTCTTAAATATATTATGTTGATGA 497

QY 2930 ACCAACAGCTGGAATGACCCCTGCTCTCGACATATTGTATGGAATCTTTTAA 2982
DB 498 AGCGACAAGTGTCTGTGATCCAGTACTACAGCTCAATTTTAAATTTATTA 550

RESULT 9
US-09-107-532A-412
; Sequence 412, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC

; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 412:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...774
; SEQUENCE DESCRIPTION: SEQ ID NO: 412:
US-09-107-532A-412

Query Match 1.1%; Score 75; DB 4; Length 774;
Best Local Similarity 47.0%; Pred. No. 6.7e-08;
Matches 302; Conservative 0; Mismatches 335; Indels 6; Gaps 2;

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QY 4994 CTTTGGACTATTGGGTCCAAATGGTCTGCGCAAAAGCAAAATATTAAATTTCTGGTTGG 5053
DB 117 TTTTGGATTTTAGGACATAATGTCGCGGAAATCAACTACGATTAAAGATTTAGTTAG 176

QY 5054 TGATATTGAACCAACTTCAGGCCAGGTATTTTAGAGATATTCTTCAGAGACAAGTGA 5113
DB 177 TATTATTGAACCATCATCGGGAACGATTTTAGTAGATGGAATGAAATTTGACGGAATCG 236

QY 5114 AGATGATGATTCACTCAAGTGTATGGTTACTGTCTCTCAGATAAACCCCTTTGTGGCCGA 5173
DB 237 ATTGAGTATCAAAACAAA---AATCGGTATGTGCTGATTTCCCGAGATATTTTTTACA 293

QY 5174 TACTACATTCAGGAACATTTTGAAATTTATGAGCTGTCAAAAGGAATGAGTCAAGTGA 5233
DB 294 ATTGACGGCTGGAGATATTGGGACTTGTATTCAGCTGCCTATGATATAGACACACAAA 353

QY 5234 CATGAAAGAGTCATTAAGTCGAATAACATGCACTTTGATTAAAAAGAACATCTTCAGAA 5293
DB 354 AAAAGAAAAAGCGTTTAGCAGATTGACAGCGCTTTTGTATATGTATGATCATCAAAATGA 413

QY 5294 GACTGTAAAGAAACTACCTCGCAGGAATCAAAAGAAAGTTGTGTTTGTCTTAAGTATGCT 5353
DB 414 AACAAATCGCAAGTTTTCACATGGAATCGGTCAAAAACCAATTTGATCGGCACGTTGCT 473

QY 5354 AGGGAATCTCTCAGATTACTTTTGTAGATGAACCATCTACAGGTATGATCCCAAGCAAA 5413
DB 474 GCAGATCCAGATATTTTGGGTATTGGTGAACCTTTTGAAGGACTTGATCTCTCAGCAGC 533

QY 5414 ACAGCACATGTGGCGGACAAATTCGAATTTAAATAACAGAAAGCGGCTGTATTTCT 5473
DB 534 ATTTGATTTGAAAGAAATGATGAAGGCTCATGCGCAAAAGGAAA---AACAGTCAATTT 590

LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1602912)..(1602912)
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LOCATION: (1603734)..(1603734)
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LOCATION: (1637998)..(1637998)
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LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g

US-08-916-421B-1

Query Match 1.1%; Score 74.6; DB 4; Length 1664976;
Best Local Similarity 49.0%; Pred. No. 1.3e-06;
Matches 259; Conservative 0; Mismatches 264; Indels 6; Gaps 2;
QY 2493 GAGCTTTGAGAAATTTGTCATTTGACATATATAGGGTGCAGATTACTGCTTACTTGGC 2552
DB 444438 GCGGTTTTAAAGGAATAAATTTTAAAGTAAAGGAGGAATGGTCTCTTTACTCGGC 444497
QY 2553 CACAGTGGACGAGAGAGTACATTGATGATATTTCTTTGTGGACTCTGCCACCTTCT 2612
DB 444498 CCTAATGGAGCTGGAAATCAACCTTTATTTTACCTTCAATGGAATTTCTAAGACCTACA 444557
QY 2613 GATGGGTTGCATCTATATATGG---ACACAGAGTCTCAGAAATAGATGAAATGTTTGA 2669
DB 444558 AAGGAGAGGTTTAAATAAGGCAAGCAATTAATATATATAAAGAAAGCTTGGTGAA 444617
QY 2670 GCAAGAAAAATGATGG---CATTTGTCCAGTTAGATATACATTTGATGTTTGTGACA 2726
DB 444618 GTTAGAAGACGGTTGATGTTGTTTTCAGAAATCCCGATGATCAGATATTTGCCCTTACA 444677
QY 2727 GTAGAAGAAATTTATCAATTTTGGCTTCAATCAAGGGATACAGCAATATATA 2786
DB 444678 GTTAAGGAGGACGCTGGCAATTTGGACCTTTAAATCTTGGCTTGCCTAAAGAAAGATTTGAG 444737
QY 2787 CAAGAAGTCAGAGGTTTTACTAGATTTAGACATGACAGACTATCAAGATAACCAAGCT 2846
DB 444738 AAGAGGTTTAAGAGGCGTTTAAAGCTGTAGGAATGGAAGTTTGAATAAATCAACCTCCT 444797
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Db 444858 CCGAGGTTATTGTTTGGATGAACCAACAGCTGGCTTAGACCTGTTGGAGCATCAAA 444917
QY 2967 GTATGAAATCTTTTAAATACAGAAAGCAATCGGGTGACAGTGTTC 3015
Db 444918 ATAATGAAATCTTATACGATTGTAATAAAAGGCGATGACCAATAATA 444966

RESULT 11

US-09-107-532A-1681
Sequence 1681, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1681:
SEQUENCE CHARACTERISTICS:
LENGTH: 768 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
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US-09-107-532A-1681

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Best Local Similarity 48.5%; Pred. No. 2.9e-07;
Matches 237; Conservative 0; Mismatches 243; Indels 9; Gaps 1;
QY 2472 AGAAAGAGGTGAAATGAGGCTTTGAGAAATTTGTCATTTGACATATATAGGGT 2531
Db 61 AAAAAAATGAGAAAGAGCGAAGCATTTAAGCGGCATCAGCTTCGATGTAGAAAAAGGC 120
QY 2532 CAGATTACTGCCCTTACTTGGCCACAGTGGAAACAGGAAAGATGATGATGATATCTTT 2591

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Db      121 GAATTTATGGGATCATGGCGCTTCTGGTTAAAGTCGACACTTTTGAATATTTTA 180
Qy      2592 TGTGGACTCTGCCACCTTCTGTATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAA 2651
Db      181 TCCACATTAGATAAACCAACAGATGGGCATATCCGAATCAATCAAAAGATGTGACCA 240
Qy      2652 ATAGATCAAAATGTTTGAAGCAAGA-----AAAATGATTGGCATTTCGCACAGTTA 2702
Db      241 TTAAGAAGAAATCACTAGACAGATTTTCGTGCGAATGAGATTGGCTTTATTTTCCAGAT 300
Qy      2703 GATATACACTTTGATGTTTTCACAGTAGAAGAAATTTATCAATTTTGGCTTCAATCAAA 2762
Db      301 TTCAATTTATTAGAAAGCTTGACAGCACAAGAAATATCGTGTCTCTCTTTTACAA 360
Qy      2763 GGGATACAGCAACAATATTAACAAGAGTGCAGAGGTTTACTAGATTTAGACATG 2822
Db      361 GCGCTCAGACCAAAAGAAATCAAGCAACGTTCCAAAAAATTCGAGAACGTTTATCCATC 420
Qy      2823 CAGACTATCAAGATACCAAGCTAAATAAATTAAGTGTGTCTCAAAAAAGAAAGCTGTCA 2882
Db      421 TCTCATATTTTGGAAAGCTATCTCTGAGATTTCCGGTGGACAAAAACACGGTCCGC 480
Qy      2883 TTAGGAATGCTGTCTTGGGAACCCAAAGATCTGCTGTAGATGAACCAACAGCTGGA 2942
Db      481 GCGCACGTGCATTGATCACACACCAACGATTCTATTAGGGATGAGCCTACAGGTGCG 540
Qy      2943 ATGGACCCC 2951
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RESULT 12

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; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6503729
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
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; US-08-916-421B-1

Query Match 1.1%; Score 71; DB 4; Length 1664976;
Best Local Similarity 46.4%; Pred. No. 8.7e-06;
Matches 276; Conservative 0; Mismatches 310; Indels 9; Gaps 1;

Qy 2430 GGAAGAAGCCATAAGAAATAGTGGTATTCAGAGACATACAGAAAGAGGGTGAAT 2489
Db 1656126 GGAATAATTTTGTAGAGAAATCTATGGTAAAGGGAGCAAAA 1656067

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Db 1656066 ACCATAGCTTTAAAAAATATTAATTTAAAAAATGAAGAGGAGAGTTGTAATGATAATG 1656007
Qy 2550 GGCCACAGTGGACAGAAAGAGTACATTCATCAATATTTCTTTGTGGACTCTGCCACCT 2609
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Qy 2610 TCTGATGGGTTTGCATCTATATATGACACAGAGTCTCGAAAAATAGATAAATGTTTGA 2669
Db 1655946 ACAAGGGGAGGCTTTATTATATAAGGGAGAGAAACAAGTTCAATGAGTGAATGAAGG 1655887
Qy 2670 GCAAGAAAAATGATTCGCATTTGTCACAGTTAGATATACATTTGATGTTTTGACAGTA 2729
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Qy 2730 GAAGAAAAATTTCAATTTTGGCTTCAATCAAAAGGATACCCAGCAACATATAATACAA 2789
Db 1655826 TTAAACAGCCTTAGAAAATGTTGAATTTACCAATGATGTTAGATGAGAGATAAGATTAT 1655767
Qy 2790 GAAGTGCAGAAAGGTTTTTACTAGATTTAGACATGCAGACTATCAAGATA-----AC 2840
Db 1655766 AGAAGGAAGAGGGCAAAAAGCTTTTGGAGATGGTTGGTAGATAGTTGAATCAT 1655707
Qy 2841 CAAGCTAAAAAATTAAGTGTGTGTCAAAAAGAAAGCTGTCTATAGAAATGCTGTTCTT 2900
Db 1655706 TACCTTCATCAATTTGAGTGGAGGGCAACAAAGAGATTGCTATAGCAAGGGCTTTAGCA 1655647
Qy 2901 GGGAACCCAAAGATAGTCTGTAGATGAACCAAGCTGGAATGGACCCCTGTTCTCGA 2960
Db 1655646 AACACCCAAAAATAATTTGCTGATGAGCCAAAGAAATTTGGACAGCAAAAGTGA 1655587
Qy 2961 CATATTGTATGGAATCTTTTAAAAATACAGAAAAACCAATCGGTGACAGTGTTC 3015
Db 1655586 ATGGCTGTTATGAGTATCTTTAAAGGGTTGAATGAAAAGAGATAACTATAATTA 1655532

RESULT 13

US-09-107-532A-1190
; Sequence 1190, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277

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17001.769 Million cell updates/sec

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Searched: 2552756 seqs, 1349719017 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6524	100.0	6525	24	ABN89594 Human ATP-binding
2	6122.8	93.8	6369	24	AAD33648 Human TRICH-3 cDNA
3	5373.2	82.3	5475	25	AB557751 cDNA encoding nove
4	5255.8	80.5	5463	25	AB557749 cDNA encoding nove
5	5247.4	80.4	5262	24	AAD37620 Human transporter
6	4918.4	75.4	4929	24	AAD37618 Human transporter
7	4807.4	73.7	4917	25	AB557750 Coding sequence of
8	4754.8	72.9	4785	24	AAD37619 Human transporter

9	2378.8	36.5	2481	25	ABZ35938 Human secretory po
10	1789.4	27.4	3928	24	ABK35707 cDNA sequence #98
11	1722.8	26.4	1818	22	AAS63176 Human purified sec
12	1543.8	23.7	1548	24	ABK35706 cDNA sequence #97
13	1319	20.2	1506	21	AAC81717 Human secreted pro
14	1182	18.1	1346	24	ABN96909 Gene #3407 used to
15	1182	18.1	1346	24	ABL63763 Breast cancer rela
16	1182	18.1	1346	24	ABL64459 Stomach cancer rel
17	1150.4	17.6	6181	24	ABN89597 Human ATP-binding
18	1149.8	17.6	5722	25	ABZ22923 Human ABCA10 trans
19	1118.8	17.1	5981	24	ABN89596 Human ATP-binding
20	1117.2	17.1	5875	25	ABN89596 Human ABCA9 transp
21	1117.2	17.1	5018	25	ABN89596 Human ABCA9 transp
22	1090.8	16.7	5296	24	ABN89595 Human ATP-binding
23	1089.2	16.7	5211	25	AAD47363 Human transporter
24	1086	16.6	5332	24	ABQ77736 Human ABCA6 transp
25	1084.6	16.6	5680	25	ABZ22922 Human ABCA10 trans
26	982.2	15.1	1632	25	ABZ35926 Human secretory po
27	933.2	14.3	5846	25	AAD49503 Human TRICH-5 cDNA
28	930.6	14.3	4727	24	AAL44690 Human transporter
29	930.6	14.3	5149	24	AAD33675 Human TRICH-30 cDN
30	908.2	13.9	4766	24	ABV99426 Human NOV47a codin
31	907.2	13.9	5677	24	ABT10141 Human breast cance
32	901.2	13.8	5065	24	AAD33650 Human TRICH-5 cDNA
33	894.8	13.7	4798	24	ABV99425 Human NOV46a codin
34	857.8	13.1	5622	24	AAD33657 Human TRICH-12 cDN
35	670.4	10.3	740	22	AAI99204 Human excretory re
36	670.4	10.3	740	22	AAI99205 Human excretory re
37	670.4	10.3	740	22	AAI99205 Human immune/haema
38	670.4	10.3	740	22	AAK84989 Human immune/haema
39	670.4	10.3	740	22	AAI63554 Human kidney relat
40	670.4	10.3	740	22	AAI63555 Human kidney relat
41	610.2	9.4	1677	23	AA570746 DNA encoding novel
42	600	9.2	668	22	AAI99206 Human excretory re
43	600	9.2	668	22	AAK84990 Human immune/haema
44	600	9.2	668	22	AAI63556 Human kidney relat
45	539.8	8.3	4345	23	AA566371 DNA encoding novel

ALIGNMENTS

RESULT 1

ABN89594

ID ABN89594 standard; cDNA; 6525 BP.

AC ABN89594;

XX

XX 18-SEP-2002 (first entry)

DT

DE Human ATP-binding cassette transporter ABCA5 cDNA SEQ ID NO:1.

XX

XX Human; ABCA5; ABCA6; ABCA9; ABCA10; ATP-binding cassette transporter;
XX chromosome 17; chromosome 17q; chromosome 17q24; antiarteriosclerotic;
XX gene therapy; cholesterol; lipophilic molecule; inflammation;
XX prostaglandin; prostacyclin; arteriosclerosis; transport; gene; ss.

XX Homo sapiens.

OS

XX WO200246458-A2.

PN

XX 13-JUN-2002.

PD

XX 07-DEC-2001; 2001WO-EP15401.

PF

XX 07-DEC-2000; 2000EP-0403440.

PR

XX 23-JAN-2001; 2001US-263231P.

PR

XX (AVET) AVENTIS PHARMA SA.

PA

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

XX Denefle P, Rosier-Montus M, Prades C, Arnould-Reguigne I;

PI

PI Duverger N, Allikmets R, Dean M;

1681 ACCTAGTTATAGCATTTTCACTTTTGGATACCTTTTGGCAATTCATATCGTAGCAGAAA 1740
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3781 ATATCAGTGTATCTTATTTAGCTTTTTCACAGCCAGACATATGTTGAGTGAATTAAG 3840
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Db 3841 ACAGTGACTATGATCGTGGCTCCCATAGTGGGCTTTAAATGATGATGCAATTCAGAAA 3900
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Db 3901 AGGACTATGTTTTGAGCTGTTTTCAAGTACTATGTTTTATCTTTACCTATATTAG 3960
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Db 4081 AAGCAGCTTTGCTTGGAAATCAATGTTACTGCAATGCCACTTACTTTGGCAATGGAAATG 4140
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Db 1848 TTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTAAATTTAAATAT 1907
Qy 1681 ACCTAGTTATAGCATTTTCCACTTTTGGATACTTTTGGCAATTCATATCGTAGCAGAAA 1740
Db 1908 ACCTAGTTATAGCATTTTCCACTTTTGGATACTTTTGGCAATTCATATCGTAGCAGAAA 1967
Qy 1741 AAGAAAAAATAAAGAAATTTTAAAGATTAATGGGACTTCATGATACTGCTTTTGGC 1800
Db 1968 AAGAAAAAATAAAGAAATTTTAAAGATTAATGGGACTTCATGATACTGCTTTTGGC 2027
Qy 1801 TTTTCTGCTGCTTCTTATATACAGTTTAAATTTTCTTATGCTTCTTATGGCAGTCA 1860
Db 2028 TTTTCTGCTGCTTCTTATATACAGTTTAAATTTTCTTATGCTTCTTATGGCAGTCA 2087
Qy 1861 TTGCGACAGCTTCTTTTGTATTTCTCAGAGTACAGCAATTTGTGATATTTCTGCTTTTTT 1920
Db 2088 TTGCGACAGCTTCTTTTGTATTTCTCAGAGTACAGCAATTTGTGATATTTCTGCTTTTTT 2147
Qy 1921 TCTTTATGGAATATCATCTGATTTTGTGTTTAAATGCTGACACTCTTTTAAATAAT 1980
Db 2148 TCTTTATGGAATATCATCTGATTTTGTGCTTTTAAATGCTGACACTCTTTTAAATAAT 2207
Qy 1981 CAABACATGCGGAATAGTTGAATTTTGTACTGTGCTTTTGGATTTATGCGCTTA 2040
Db 2208 CAABACATGCGGAATAGTTGAATTTTGTACTGTGCTTTTGGATTTATGCGCTTA 2267
Qy 2041 TGATAATCCTCATAGAAAGTTTTCCTCAATCGTTAGTGTGCTTTTTCAGTCTTTTCTGTC 2100
Db 2268 TGATAATCCTCATAGAAAGTTTTCCTCAATCGTTAGTGTGCTTTTTCAGTCTTTTCTGTC 2327
Qy 2101 ACTGTACTTTTGTGATTTGGTATTTGACAGGTCATGCAATTTAGAAATTTAATGAGGTG 2160
Db 2328 ACTGTACTTTTGTGATTTGGTATTTGACAGGTCATGCAATTTAGAAATTTAATGAGGTG 2387
Qy 2161 CTTTCAATTTCAATTTGACTGCGGCCCATATCCCTTAATTTAATTAATTAATCATGCTCA 2220
Db 2388 CTTTCAATTTCAATTTGACTGCGGCCCATATCCCTTAATTTAATTAATTAATCATGCTCA 2447
Qy 2221 CACTTAATAGTATATTTATGTCCTCTTGGCTGTCTATCTTGTATCAAGTCAATTCAGGGG 2280
Db 2448 CACTTAATAGTATATTTATGTCCTCTTGGCTGTCTATCTTGTATCAAGTCAATTCAGGGG 2507
Qy 2281 AATTTGGCTTACGGAGATCATCTTTTATATTTTCTGAGGCTTCATATTTGGTCAAGAGTA 2340
Db 2508 AATTTGGCTTACGGAGATCATCTTTTATATATTTTCTGAGGCTTCATATTTGGTCAAGAGTA 2567

QY 2341 AAAGAAATATGAGGAGTATCAGAGGCAATGTTAATGAAATATATAGTTTTAGTGA 2400
DB 2568 AAAGAAATATGAGGAGTATCAGAGGCAATGTTAATGAAATATATAGTTTTAGTGA 2627
QY 2401 TTATGTAGCCAGTTTCTTCAGAAATTTGTAGAAAGAGCCATGAAGATTTAGTGGTATTC 2460
DB 2628 TTATGTAGCCAGTTTCTTCAGAAATTTGTAGAAAGAGCCATGAAGATTTAGTGGTATTC 2687
QY 2461 AGAAGACATACAGAAAGAGGTCGAAATGTTGAGAGGCTTTGAGAAATTTGTCATTTCACA 2520
DB 2688 AGAAGACATACAGAAAGAGGTCGAAATGTTGAGAGGCTTTGAGAAATTTGTCATTTCACA 2747
QY 2521 TATATGAGGTCAGATTAATGTCCTTACTTGGCCACAGTGGAAACAGGAAAGAGTACATTGA 2580
DB 2748 TATATGAGGTCAGATTAATGTCCTTACTTGGCCACAGTGGAAACAGGAAAGAGTACATTGA 2807
QY 2581 TGAATATTTCTTTGGGACTGTCGCCACCTTCTGATGGGTTTGATCTATATATGAGACACA 2640
DB 2808 TGAATATTTCTTTGGGACTGTCGCCACCTTCTGATGGGTTTGATCTATATATGAGACACA 2867
QY 2641 GAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAATGATTTGGCATTTGTCACAGT 2700
DB 2868 GAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAATGATTTGGCATTTGTCACAGT 2927
QY 2701 TAGATATACATTTGATGTTTGTGACAGTGAAGAAATTTATCAATTTTGGCTTCAATCA 2760
DB 2928 TAGATATACATTTGATGTTTGTGACAGTGAAGAAATTTATCAATTTTGGCTTCAATCA 2987
QY 2761 AAGGGATACCAAGCAACAATATAACAAGAGTGCAGAGGTTTACTAGATTTAGACA 2820
DB 2988 AAGGGATACCAAGCAACAATATAACAAGAGTGCAGAGGTTTACTAGATTTAGACA 3047
QY 2821 TGCAGACTATCAAGATTAACAAGCTAAATTAAGTGGTGGTCAAAAAGAAAGCTGT 2880
DB 3048 TGCAGACTATCAAGATTAACAAGCTAAATTAAGTGGTGGTCAAAAAGAAAGCTGT 3107
QY 2881 CATTAGGAATGCTGTTCTTGGGAACCAAGATACCTGCTAGATGAACCAACAGCTG 2940
DB 3108 CATTAGGAATGCTGTTCTTGGGAACCAAGATACCTGCTAGATGAACCAACAGCTG 3167
QY 2941 GAATGGACCCCTGTTCTGACATATGATGGAATCTTTTAAATAACAGAAAGCCAAATC 3000
DB 3168 GAATGGACCCCTGTTCTGACATATGATGGAATCTTTTAAATAACAGAAAGCCAAATC 3227
QY 3001 GGGTGACAGTGTTCAGTACTCATTTTCATGATGAAGCTGACATTTCTTGCAGATAGGAAG 3060
DB 3228 GGGTGACAGTGTTCAGTACTCATTTTCATGATGAAGCTGACATTTCTTGCAGATAGGAAG 3287
QY 3061 CTGTGATATCAAGGAATGCTGAAATGTTGTTGGTCTTCAATGTTCTCAAAAGTAAAT 3120
DB 3288 CTGTGATATCAAGGAATGCTGAAATGTTGTTGGTCTTCAATGTTCTCAAAAGTAAAT 3347
QY 3121 GGGGGATCGGCTACCGCTGAGCATGACATGACAAATATTTGTCACAGAAATCTCTTT 3180
DB 3348 GGGGGATCGGCTACCGCTGAGCATGACATGACAAATATTTGTCACAGAAATCTCTTT 3407
QY 3181 CTTTCACTGGTTAAACAATATACCTGAGCTACTTTTATACACAGAAATGACCAACAC 3240
DB 3408 CTTTCACTGGTTAAACAATATACCTGAGCTACTTTTATACACAGAAATGACCAACAC 3467
QY 3241 TTGTGATAGCTGCTGCTTTCAAGGACATGGACAAATTTTCAAGTTTCTGTCGCCCTAG 3300
DB 3468 TTGTGATAGCTGCTGCTTTCAAGGACATGGACAAATTTTCAAGTTTCTGTCGCCCTAG 3527
QY 3301 ACAGTCAATCAAAATTTGGGTGTCATTTCTTATGTTGTTTCCATGACGACTTTGGAAGACG 3360
DB 3528 ACAGTCAATCAAAATTTGGGTGTCATTTCTTATGTTGTTTCCATGACGACTTTGGAAGACG 3587
QY 3361 TATTTTTAAGCTAGAGTTGAAGCAGAAATTTGACCAAGCATTTATAGTGTATTTACTC 3420
DB 3588 TATTTTTAAGCTAGAGTTGAAGCAGAAATTTGACCAAGCATTTATAGTGTATTTACTC 3647

QY 3421 AGCAGCCACTGGAGGAAGAAATGGAATTTCAAAATCTTTTGTGATGAATGGAACAGAGCTTAC 3480
DB 3648 AGCAGCCACTGGAGGAAGAAATGGAATTTCAAAATCTTTTGTGATGAATGGAACAGAGCTTAC 3707
QY 3481 TTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAAGCACCATGAGCCTTTGGAAACAACAGA 3540
DB 3708 TTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAAGCACCATGAGCCTTTGGAAACAACAGA 3767
QY 3541 TGTATACAAATAGCAAAAGTTTTCATTTCTTTTACCTTGAACCTGAAAGTAAATCAGTGAAT 3600
DB 3768 TGTATACAAATAGCAAAAGTTTTCATTTCTTTTACCTTGAACCTGAAAGTAAATCAGTGAAT 3827
QY 3601 CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTGTTGCTCATC 3660
DB 3828 CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTGTTGCTCATC 3887
QY 3661 ACTCTTTTAAATAGTGTGCTTCCCATCAAACTGTTCCAGACTTATATTTCTTAAAC 3720
DB 3888 ACTCTTTTAAATAGTGTGCTTCCCATCAAACTGTTCCAGACTTATATTTCTTAAAC 3947
QY 3721 CTGGAGACAAACCAACATAAATACAAAACAAAGTCTGCTTCTTCAAAATTTCTGCTGACTCAG 3780
DB 3948 CTGGAGACAAACCAACATAAATACAAAACAAAGTCTGCTTCTTCAAAATTTCTGCTGACTCAG 4007
QY 3781 ATATCAGTGAATCTTATTTAGCTTTTTCACAAAGCCAGAACATAATGTTGACGATGATTAATG 3840
DB 4008 ATATCAGTGAATCTTATTTAGCTTTTTCACAAAGCCAGAACATAATGTTGACGATGATTAATG 4067
QY 3841 ACAGTGAATGATGATCCGTGGCTCCCATAGTGGGCTTTAAATGTTGATGATGATTTAGAAA 3900
DB 4068 ACAGTGAATGATGATCCGTGGCTCCCATAGTGGGCTTTAAATGTTGATGATGATTTAGAAA 4127
QY 3901 AGGACTATGTTTTGAGCTGTTTTCAACAGTACTATGTTTTATTTCTTCACTTATATTTAG 3960
DB 4128 AGGACTATGTTTTGAGCTGTTTTCAACAGTACTATGTTTTATTTCTTACCTATATTTAG 4187
QY 3961 TGAATATCAATTAGTAATCTACTCTTTTATCATTTAAATGTGACTGAAACCATCCAGATCT 4020
DB 4188 TGAATATCAATTAGTAATCTACTCTTTTATCATTTAAATGTGACTGAAACCATCCAGATCT 4247
QY 4021 GGAGTACCCCATCTTTTCAAGAAATTAATCTGATATAGTTTTTAAATGTTGATGATTTTTC 4080
DB 4248 GGAGTACCCCATCTTTTCAAGAAATTAATCTGATATAGTTTTTAAATGTTGATGATTTTTC 4307
QY 4081 AAGCAGCTTGTCTGGAATCATTTGTTACTGCAATGCCACTTACTTGGCCATGAAATG 4140
DB 4308 AAGCAGCTTGTCTGGAATCATTTGTTACTGCAATGCCACTTACTTGGCCATGAAATG 4367
QY 4141 CAGAGAAATCATAGATCAAGGCTTATACTCAACTTAAACCTTTTCCAGGTCTTTTGGCCATCTG 4200
DB 4368 CAGAGAAATCATAGATCAAGGCTTATACTCAACTTAAACCTTTTCCAGGTCTTTTGGCCATCTG 4427
QY 4201 CATATTTGGAATGGAAGCTGTTGTTGATATCCCTTTATTTTATCATTTCTTATTTTGA 4260
DB 4428 CATATTTGGAATGGAAGCTGTTGTTGATATCCCTTTATTTTATCATTTCTTATTTTGA 4487
QY 4261 TGTCTAGAGGCTTACTGGAATTTTCAATGGAATATATTTTATATCTGTAAGTCCCTG 4320
DB 4488 TGTCTAGAGGCTTACTGGAATTTTCAATGGAATATATTTTATATCTGTAAGTCCCTG 4547
QY 4321 CTGTGGTTTTTGGCTTATTTGGTTATGTTCCATCAGTATTTCTGTTCACTTATATTTGCTT 4380
DB 4548 CTGTGGTTTTTGGCTTATTTGGTTATGTTCCATCAGTATTTCTGTTCACTTATATTTGCTT 4607
QY 4381 CTTTCACTTTTAAAGAAATTTTAAATAACAAAGAAATTTTGGTCAATTTATCTATCTGTGG 4440
DB 4608 CTTTCACTTTTAAAGAAATTTTAAATAACAAAGAAATTTTGGTCAATTTATCTATCTGTGG 4667
QY 4441 CAGCGTTGCTGTTATGCAATCAGTGAATTAATCTTTTATGGATAGACAAATTTGCA 4500
DB 4668 CAGCGTTGCTGTTATGCAATCAGTGAATTAATCTTTTATGGATAGACAAATTTGCA 4727
QY 4501 CTATTTCTTCAATTTGCTTTTGTATCATCATTTCCAATCTATCCAATTTCTAGGTTGCTGCA 4560

Db	4728	 CTATTCTTCATATATGCGCTTTTGTATCATCATATCCAATCTATCCACTTCTAGGTGGCTGA	4787
Qy	4561	 TTTCTTTTCATTAAGATTTCTTTGGAGAAGATGTCAGAAAAAATGTGGACACCTATAATCCCAT	4620
Db	4788	 TTTCTTTTCATTAAGATTTCTTTGGAGAAGATGTCAGAAAAAATGTGGACACCTATAATCCCAT	4847
Qy	4621	 GGGATAGGCTTTTCAGTAGCTGTTATATCGGCTTTACCTGCGAGTGTGTACTGTGGATTTTCC	4680
Db	4848	 GGGATAGGCTTTTCAGTAGCTGTTATATCGGCTTTACCTGCGAGTGTGTACTGTGGATTTTCC	4907
Qy	4681	 TCTTACAATTAATGAGAAAAAATATGGAGGCGAGATCAATAAGAAAAAGATCCCTTTTTC	4740
Db	4908	 TCTTACAATTAATGAGAAAAAATATGGAGGCGAGATCAATAAGAAAAAGATCCCTTTTTC	4967
Qy	4741	 GAAACCTTTCAACGAAGTCTTAAATAAGGAAGCTTCCAGAACACCCAGACAAATGAGGATG	4800
Db	4968	 GAAACCTTTCAACGAAGTCTTAAATAAGGAAGCTTCCAGAACACCCAGACAAATGAGGATG	5027
Qy	4801	 AAGATGAAGATGTCAAAAGCTGAAAGACTTAAAGGTCAAAAGAGCTGATGGGTTCGCAGTGT	4860
Db	5028	 AAGATGAAGATGTCAAAAGCTGAAAGACTTAAAGGTCAAAAGAGCTGATGGGTTCGCAGTGT	5087
Qy	4861	 GTGAGGAGAAACCATCCATTATGGTCAAGCAATTTTGCATAAAGAAATATGATGACAAGAAAG	4920
Db	5088	 GTGAGGAGAAACCATCCATTATGGTCAAGCAATTTTGCATAAAGAAATATGATGACAAGAAAG	5147
Qy	4921	 ATTTTCTTTTCAAGAAAAAGTAAAGAGTGGCACTTAATATCATCTCTTTCTGTGTGA	4980
Db	5148	 ATTTTCTTTTCAAGAAAAAGTAAAGAGTGGCACTTAATATCATCTCTTTCTGTGTGA	5207
Qy	4981	 AAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGCACAAATATTATTA	5040
Db	5208	 AAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGCACAAATATTATTA	5267
Qy	5041	 ATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTATAGGAGATTAATTCCT	5100
Db	5268	 ATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTATAGGAGATTAATTCCT	5327
Qy	5101	 CAGAGACAAGTGAAGATGATGATTCACCTGAAGTGTATGGGTACTGCTCCACAGATAAAC	5160
Db	5328	 CAGAGACAAGTGAAGATGATGATTCACCTGAAGTGTATGGGTACTGCTCCACAGATAAAC	5387
Qy	5161	 CTTTGTGGCCAGATACACATTCAGAGAAACATTTTGAATTTATGGAGCTGTCAAAAGGAA	5220
Db	5388	 CTTTGTGGCCAGATACACATTCAGAGAAACATTTTGAATTTATGGAGCTGTCAAAAGGAA	5447
Qy	5221	 TGAGTCAAGTGACATGAAGAGTCAATAAGTCGAATTAACACATGCACTTGAATTTAAAG	5280
Db	5448	 TGAGTCAAGTGACATGAAGAGTCAATAAGTCGAATTAACACATGCACTTGAATTTAAAG	5507
Qy	5281	 AACATCTTCAGAGACGTGAAGAAACTACCTGCAGGAATCAACAGAAAGTTGTGTTTG	5340
Db	5508	 AACATCTTCAGAGACGTGAAGAAACTACCTGCAGGAATCAACAGAAAGTTGTGTTTG	5567
Qy	5341	 CTCTAAGTATGCTAGGGAATCCTCAGATTAATTTTGTAGATGAACCACTACAGGTATGG	5400
Db	5568	 CTCTAAGTATGCTAGGGAATCCTCAGATTAATTTTGTAGATGAACCACTACAGGTATGG	5627
Qy	5401	 ATCCCAAGGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCAATTTAAAAACAGAAAGC	5460
Db	5628	 ATCCCAAGGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCAATTTAAAAACAGAAAGC	5687
Qy	5461	 GGGCTGCTATTGCAACACTCATATATGAGGAGGAGGAGGCTGTCTGTGATCGAGTAG	5520
Db	5688	 GGGCTGCTATTGCAACACTCATATATGAGGAGGAGGAGGCTGTCTGTGATCGAGTAG	5747
Qy	5521	 CTATCATGTGTCTGGGCGAGTTAAGATGTATCGGAAACAGTACAACATCTTAAAGAGTAAAT	5580
Db	5748	 CTATCATGTGTCTGGGCGAGTTAAGATGTATCGGAAACAGTACAACATCTTAAAGAGTAAAT	5807
Qy	5581	 TTGGAAAGGGCTACTTTTGTGAAATTTAAATTTGAAGGACTGGATAGAAAAACCTAGAGTAG	5640

Db	5808	TTGGAAAGAGCTACTTTTGTGGAAATTAATAATTGAAGGAGCTGGATAGAAAACCTTAGAAGTAG	586
Qy	5641	ACGCGCTTCAAAGAGAAATTCAGTATATTTTCCAAATGCAAGCCGTCAGGAAAAGTTTTT	5700
Db	5868	ACGCGCTTCAAAGAGAAATTCAGTATATTTTCCAAATGCAAGCCGTCAGGAAAAGTTTTT	5927
Qy	5701	CTTCTATTTTGGCTTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCACAATCTTTTT	5760
Db	5928	CTTCTATTTTGGCTTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCACAATCTTTTT	5987
Qy	5761	TTAAGCTGGGAAGAGCTAATCATGCTTTTCCCAATTTGAAGAATATAGCTTTTCTCAAGCAA	5820
Db	5988	TTAAGCTGGGAAGAGCTAATCATGCTTTTCCCAATTTGAAGAATATAGCTTTTCTCAAGCAA	6047
Qy	5821	CAATTGGAAACAGGTTTTTTGTAGAACTCACTAAAGAAACAAGAGGAGGAGATAATAGTTGTG	5880
Db	6048	CAATTGGAAACAGGTTTTTTGTAGAACTCACTAAAGAAACAAGAGGAGGAGATAATAGTTGTG	6107
Qy	5881	GAACTTTAAACAGCACACTTTTGTGGGAACGAACAACAAGAAGATAGAGTAGTATTTTGAA	5940
Db	6108	GAACTTTAAACAGCACACTTTTGTGGGAACGAACAACAAGAAGATAGAGTAGTATTTTGAA	6167
Qy	5941	TTTGTATTTGTCGGTCTGCTTACTGGGACCTCTTCTTTTCACTTAATTTTAACTTTTG	6000
Db	6168	TTTGTATTTGTCGGTCTGCTTACTGGGACCTCTTCTTTTCACTTAATTTTAACTTTTG	6227
Qy	6001	TTTAAAAAGTTTTTTTTTATTTGGAATGGTAACTGGAGAACCAAGAACCGCACTTTGAAATTTTC	6060
Db	6228	TTTAAAAAGTTTTTTTTTATTTGGAATGGTAACTGGAGAACCAAGAACCGCACTTTGAAATTTTC	6287
Qy	6061	TAAGCTCCTTAAATGAAAGCTGTGGTGTGTGTTTGTCTTTCTTTAAATAAAACGTAT	6120
Db	6288	TAAGCTCCTTAAATGAAAGCTGTGGTGTGTGTTTGTCTTTCTTTAAATAAAACGTAT	6347
Qy	6121	GTATAATTAAGTGAA	6135
Db	6348	GTATAATTAAGTGAA	6362
RESULT 3			
ABS57751			
ID	ABS57751 standard; cDNA; 5475 BP.		
XX	AC	ABS57751;	
XX	AC	ABS57751;	
DT	04-FEB-2003	(first entry)	
XX	cDNA encoding novel human ATP binding cassette ABCA5 transporter #2.		
DE	Human; ATP binding cassette; ABC; ABCA5; transporter;		
KW	neurotoxin transport; beta-amyloid peptide; chromosome mapping;		
KW	blood brain barrier transport; tissue typing; predictive medicine;		
KW	ABCA5 mediated disorder; ABCA5 related disorder; gene therapy;		
KW	gene; ss.		
XX	OS	Homo sapiens.	
XX	OS	Homo sapiens.	
FH	Key	Location/Qualifiers	
FT	CDS	114..5042	
FT	/*tag= a		
FT	/product= "ABCA5"		
FT	/note= "ATP binding cassette (ABC) A5 transporter"		
XX			
FN	US2002123107-A1.		
XX			
PD	05-SEP-2002.		
XX			
PF	01-MAR-2002; 2002US-0090458.		
XX			
PR	02-MAR-2001; 2001US-272885P.		
XX			
PA	(ACTI-) ACTIVE PASS PHARM INC.		
XX			

[illegible]

QY	4714	GATCAATAAGAAAGATCCCTTTTTCAGAAACCTTTCAACGAAGCTCTAAATAATAGGAAGC	4773
DB	3817	GATCAATAAGAAAGATCCCTTTTTCAGAAACCTTTCAACGAAGCTCTAAATAATAGGAAGC	3876
QY	4774	TTCCAGAACCAACAGCAATGAGGATGAAGATGAAGATGTCAGAGCTGGAAGCTAAAGG	4833
DB	3877	TTCCAGAACCAACAGCAATGAGGATGAAGATGAAGATGTCAGAGCTGGAAGCTAAAGG	3936
QY	4834	TCAAGAGCTGATGGGTTCAGAGTGTGAGAGAAACCATCCATTTATGGTCAGCAAT	4893
DB	3937	TCAAGAGCTGATGGGTTCAGAGTGTGAGAGAAACCATCCATTTATGGTCAGCAAT	3996
QY	4894	TGCATTAAGAAATATGATGACAAAGATTTTCTTCTTCAAGAAAGTAAAGAAAGTGG	4953
DB	3997	TGCATTAAGAAATATGATGACAAAGATTTTCTTCTTCAAGAAAGTAAAGAAAGTGG	4056
QY	4954	CAACTAAATACATCTCTTCTGTCGTAAGAAAGGAGAGATCTTAGAGCTATTGGGTCCAA	5013
DB	4057	CAACTAAATACATCTCTTCTGTCGTAAGAAAGGAGAGATCTTAGAGCTATTGGGTCCAA	4116
QY	5014	ATGGTGTGTCGCAAAAGCACAAATTAATTAATTTCTGGTGGTGATATTGAACCAACTTCAG	5073
DB	4117	ATGGTGTGTCGCAAAAGCACAAATTAATTAATTTCTGGTGGTGATATTGAACCAACTTCAG	4176
QY	5074	GCCAGGATTTTATGAGATATTCTTTCAGAGCAAGTGAAGATGATTCACCTGAAGT	5133
DB	4177	GCCAGGATTTTATGAGATATTCTTTCAGAGCAAGTGAAGATGATTCACCTGAAGT	4236
QY	5134	GTATGGGTACTCTCTCAGATAAACCCCTTTGTGGCCAGATACATATTCAGGAAACAT	5193
DB	4237	GTATGGGTACTCTCTCAGATAAACCCCTTTGTGGCCAGATACATATTCAGGAAACAT	4296
QY	5194	TTGAAATTTATGAGCTGTCAAAAGGAATGATGCAAGTGCATGAAAGAGTCAATAGTC	5253
DB	4297	TTGAAATTTATGAGCTGTCAAAAGGAATGATGCAAGTGCATGAAAGAGTCAATAGTC	4356
QY	5254	GAATAACATGACCTGTGATTTTAAAGAAACATCTTTCAGAGATCTGTAAGAAACATCCTG	5313
DB	4357	GAATAACATGACCTGTGATTTTAAAGAAACATCTTTCAGAGATCTGTAAGAAACATCCTG	4416
QY	5314	CAGGAATCAAAACCAAGTGTGTTTCTCTAAGTATGCTAGGGAATCCTCAGATTACTT	5373
DB	4417	CAGGAATCAAAACCAAGTGTGTTTCTCTAAGTATGCTAGGGAATCCTCAGATTACTT	4476
QY	5374	TGCTAGATGAACCATCTACAGGTATGATCCCAAGCCAAACAGACATGTCGCGAGCAA	5433
DB	4477	TGCTAGATGAACCATCTACAGGTATGATCCCAAGCCAAACAGACATGTCGCGAGCAA	4536
QY	5434	TTCGAACTGCATTTAAAGAACAGAAAGCGGCTCTATTCTGACCCTCACTATATGGAGG	5493
DB	4537	TTCGAACTGCATTTAAAGAACAGAAAGCGGCTCTATTCTGACCCTCACTATATGGAGG	4596
QY	5494	AGCAGAGGCTGTCTGTATCGAGTAGCTATCATGTGTCTGGGAGTTAAGATGATCG	5553
DB	4597	AGCAGAGGCTGTCTGTATCGAGTAGCTATCATGTGTCTGGGAGTTAAGATGATCG	4656
QY	5554	GAACAGTACAACTCTAAAGAGTAAATTTGGAAGAGCTACTTTTGGAAATTAATTTGA	5613
DB	4657	GAACAGTACAACTCTAAAGAGTAAATTTGGAAGAGCTACTTTTGGAAATTAATTTGA	4716
QY	5614	AGGACTGGATAGAAACCTAGAAAGTAGACCGCCCTTCAAGAGAGAAATTCAGTATATTTCC	5673
DB	4717	AGGACTGGATAGAAACCTAGAAAGTAGACCGCCCTTCAAGAGAGAAATTCAGTATATTTCC	4776
QY	5674	CAAAATGCAAGCCGTGAGAAAGTTTCTCTATTTTGGCTTATAAAATTCCTAAGGAAG	5733
DB	4777	CAAAATGCAAGCCGTGAGAAAGTTTCTCTATTTTGGCTTATAAAATTCCTAAGGAAG	4836
QY	5734	ATGTTTCAGTCCCTTTCACAACTCTTTTAAAGCTGGAAGCTAAACATGCTTTTGCCA	5793
DB	4837	ATGTTTCAGTCCCTTTCACAACTCTTTTAAAGCTGGAAGCTAAACATGCTTTTGCCA	4896
QY	5794	TTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCACTAAAG	5853

DB	4897	TTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCACTAAAG	4956
QY	5854	AACAAGAGAGAGGAAGATAATAGTTGTGGAACTTTTAAACAGCACACTTTGTGGGAACGAA	5913
DB	4957	AACAAGAGAGAGGAAGATAATAGTTGTGGAACTTTTAAACAGCACACTTTGTGGGAACGAA	5016
QY	5914	CACAAGAGATAGAGTAGTATTTTGGAATTTGTTTCTGGTCTGCTTACTGGGACTTCT	5973
DB	5017	CACAAGAGATAGAGTAGTATTTTGGAATTTGTTTCTGGTCTGCTTACTGGGACTTCT	5076
QY	5974	TTCTTTTTCACCTTAATTTTAACTTTTGAAGTTTAAAGCTTTTATTGGAATGGTAATGGA	6033
DB	5077	TTCTTTTTCACCTTAATTTTAACTTTTGAAGTTTAAAGCTTTTATTGGAATGGTAATGGA	5136
QY	6034	GAACCAAGAACCCACCTTGAAGTTTCTTAAGCTCTTAAATTTGAAATGCTGTGGTGTG	6093
DB	5137	GAACCAAGAACCCACCTTGAAGTTTCTTAAGCTCTTAAATTTGAAATGCTGTGGTGTG	5196
QY	6094	TTTGTCTTTTCTTAAATAAACGATGATGATATTAATTAAGTGAAGCTGCATGTTGTATTGA	6153
DB	5197	TTTGTCTTTTCTTAAATAAACGATGATGATATTAATTAAGTGAAGCTGCATGTTGTATTGA	5256
QY	6154	AGTATATGAACTATATAGTTTGTATGTCATCTTTTTCACCATTCAGAAACAGTGTCT	6213
DB	5257	AGTATATGAACTATATAGTTTGTATGTCATCTTTTTCACCATTCAGAAACAGTGTCT	5316
QY	6214	GAATTTGTGATTTTAAAGGAATTTGTAATAGATAGTTTATTATTAAAGTTATCTTTAAGTT	6273
DB	5317	GAATTTGTGATTTTAAAGGAATTTGTAATAGATAGTTTATTATTAAAGTTATCTTTAAGTT	5376
QY	6274	TATGCCATCTTCTTAAATAAAGTACGTAATGTTCCAACTTAAATAAAAACTAATACATAA	6333
DB	5377	TATGCCATCTTCTTAAATAAAGTACGTAATGTTCCAACTTAAATAAAAACTAATACATAA	5436
QY	6334	CTAATGCTAGAAAAAGATACATAAAGCAATGTGAAAGTT	6372
DB	5437	CTAATGCTAGAAAAAGATACATAAAGCAATGTGAAAGTT	5475

RESULT 4
ABSS7749 standard; cDNA; 5463 BP.

XX AC ABSS7749;
XX DT 04-FEB-2003 (first entry)
XX DE cDNA encoding novel human ATP binding cassette ABCA5 transporter #1.
XX KW Human; ATP binding cassette; ABC; ABCA5; transporter;
XX KW neurotoxin transport; beta-amyloid peptide; chromosome mapping;
XX KW blood brain barrier transport; tissue typing; predictive medicine;
XX KW ABCA5 mediated disorder; ABCA5 related disorder; gene therapy;
XX KW gene; ss.
XX OS Homo sapiens.
XX FH Key
XX FT CDS
XX FT 114..5030
XX FT /*tag= a
XX FT /product= "ABCA5"
XX FT /note= "ATP binding cassette (ABC) A5 transporter"
XX FT /transl_except= (pos:3273..3275, aa:Ser)
XX US2002123107-A1.
XX PN
XX PD 05-SEP-2002.
XX PF 01-MAR-2002; 2002US-0090458.
XX PR 02-MAR-2001; 2001US-272885P.
XX XX

Qy	2494	AGGCTTTGAGAAATTTCTCAATTTGACATATATAGGGGTGAGATTA	2553	
Db	1597	AGGCTTTGAGAAATTTCTCAATTTGACATATATAGGGGTGAGATTA	1656	
Qy	2554	ACAGTGAACAGGAAGTACATTTGATGAATATTTCTTTTGACACTCTG	2613	
Db	1657	ACAGTGAACAGGAAGTACATTTGATGAATATTTCTTTTGACACTCTG	1716	
Qy	2614	ATGGGTTTGCAATCTATATATGGGACACAGAGTCTCAGAAATAGAT	2673	
Db	1717	ATGGGTTTGCAATCTATATATGGGACACAGAGTCTCAGAAATAGAT	1776	
Qy	2674	GAAAAATGATTTGGCAATTTGCTCCACAGTTAGATATACACTTTGAT	2733	
Db	1777	GAAAAATGATTTGGCAATTTGCTCCACAGTTAGATATACACTTTGAT	1836	
Qy	2734	AAAAATTTATCAATTTTGGCTTCAATCAAGGGATACAGCAACNATAT	2793	
Db	1837	AAAAATTTATCAATTTTGGCTTCAATCAAGGGATACAGCAACNATAT	1896	
Qy	2794	TGCAGAAAGGTTTACTAGATTTAGACATGCAGACTATCAAGATTAAC	2853	
Db	1897	TGCAGAAAGGTTTACTAGATTTAGACATGCAGACTATCAAGATTAAC	1956	
Qy	2854	TAAGTGTGTGTCAAAAAGAAAGCTGTCATTTAGGAATTTGCTTTTGG	2913	
Db	1957	TAAGTGTGTGTCAAAAAGAAAGCTGTCATTTAGGAATTTGCTTTTGG	2016	
Qy	2914	TACTGTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGAC	2973	
Db	2017	TACTGTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGAC	2076	
Qy	2974	ATCTTTTAAAAATACAGAAAAAGCCAAATCGGTGACAGTGTTCAGTAC	3033	
Db	2077	ATCTTTTAAAAATACAGAAAAAGCCAAATCGGTGACAGTGTTCAGTAC	2136	
Qy	3034	AAGCTGACATTTCTTTGACAGATAGGAAGCTGTGTATATCAAGGAAT	3093	
Db	2137	AAGCTGACATTTCTTTGACAGATAGGAAGCTGTGTATATCAAGGAAT	2196	
Qy	3094	GTCTTCAATTTCTCTCAAAAGTAAATGGGGGATCGGCTACCGCTGAG	3153	
Db	2197	GTCTTCAATTTCTCTCAAAAGTAAATGGGGGATCGGCTACCGCTGAG	2256	
Qy	3154	ACAAATATTTGTCACAGAAATCTCTTTCTTCACTGTTTAAACACATAT	3213	
Db	2257	ACAAATATTTGTCACAGAAATCTCTTTCTTCACTGTTTAAACACATAT	2316	
Qy	3214	CTTTATTAACAAGAAATGACCAACAACTGTGTATAGCTTTGCCCTTCA	3273	
Db	2317	CTTTATTAACAAGAAATGACCAACAACTGTGTATAGCTTTGCCCTTCA	2376	
Qy	3274	AAATTTTCAGGTTTGTCTGCCCCCTAGACATCTTCAAAATTTGGGTTG	3333	
Db	2377	AAATTTTCAGGTTTGTCTGCCCCCTAGACATCTTCAAAATTTGGGTTG	2436	
Qy	3334	GTGTTTCCATGACACCTTTGGAAGACCTATTTTAAAGCTAGAGTTGA	3393	
Db	2437	GTGTTTCCATGACACCTTTGGAAGACCTATTTTAAAGCTAGAGTTGA	2496	
Qy	3394	ACCAAGCAGATATTAGTGTATTTTACTCAGACGCCACTGGAAGGAAT	3453	
Db	2497	ACCAAGCAGATATTAGTGTATTTTACTCAGACGCCACTGGAAGGAAT	2556	
Qy	3454	CTTTTGATGAATGGAAACAGAGCTTACTTATTTCTTCTGAAACCAAG	3513	
Db	2557	CTTTTGATGAATGGAAACAGAGCTTACTTATTTCTTCTGAAACCAAG	2616	
Qy	3514	GCACATGAGCCTTTGGAACCAACAGATGTATACAAATAGCAAGTTCA	3573	
Db	2617	GCACATGAGCCTTTGGAACCAACAGATGTATACAAATAGCAAGTTCA	2676	
Qy	3574	TGAAACCTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAA	3633	

Db	2677	TGAAACCTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAA	2736	
Qy	3634	TTTCAGATTTTATGTTTGTGTTTTCATCACTCTTTTAAATGCTGTTCC	3693	
Db	2737	TTTCAGATTTTATGTTTGTGTTTTCATCACTCTTTTAAATGCTGTTCC	2796	
Qy	3694	TTGTTCCAGACCTTATATTTTCTAAAAACCTGGAGACAAACCAATAA	3753	
Db	2797	TTGTTCCAGACCTTATATTTTCTAAAAACCTGGAGACAAACCAATAA	2856	
Qy	3754	TGCTTCTTCAAAATTTCTGCT-----GACTCAGATATCAGTGATCTTA	3795	
Db	2857	TGCTTCTTCAAAATTTCTGCTGCTGAGAGTGTGNGTGAAGACTCAGAT	2916	
Qy	3796	TTAGCTTTTTCACAAGCCAGAAACATTAATGCTGACGATGATTAATGA	3855	
Db	2917	TTAGCTTTTTCACAAGCCAGAAACATTAATGCTGACGATGATTAATGA	2976	
Qy	3856	CGTGCTCCTCCCATAGTCGGGCTTTAAATGTGATGCAITTCAGAAAA	3915	
Db	2977	CGTGCTCCTCCCATAGTCGGGCTTTAAATGTGATGCAITTCAGAAAA	3036	
Qy	3916	CAGCTGTTTTCACAAGTACTATGTTTATTTCTTACCTATATTTAGTGA	3975	
Db	3037	CAGCTGTTTTCACAAGTACTATGTTTATTTCTTACCTATATTTAGTGA	3096	
Qy	3976	ACTACTACTCTTTTATCAATTTAAATGTGACCTGAACCATCCAGATCT	4035	
Db	3097	ACTACTACTCTTTTATCAATTTAAATGTGACCTGAACCATCCAGATCT	3156	
Qy	4036	TTCAAGAAATTTACTGATATAGTTTTTAAATTTGAGCTGTATTTTCAAG	4095	
Db	3157	TTCAAGAAATTTACTGATATAGTTTTTAAATTTGAGCTGTATTTTCAAG	3216	
Qy	4096	G--AATCAATTTGTTACTGCAATGCGACCTTACTTTGCCATGGAAAT	4154	
Db	3217	GAAATCAATTTGTTAACTGCAATGCGACCTACTCTGCCATGGAAAT	3274	
Qy	4155	ATCAAGCTTATACTCAACTTAACTTTTCAAGCTCTTGGCATCTGCATAT	4214	
Db	3275	-----AGGCTTTTGGCCATCTGCATATTTGGATTTGGA	3305	
Qy	4215	CAAGCTGTTTGTGATATCCCTTTATTTTATCATTTTATTTGATGCTAG	4274	
Db	3306	CAAGCTGTTTGTGATATCCCTTTATTTTATCATTTTATTTGATGCTAG	3365	
Qy	4275	CTGGCAATTTCAATTAAGGATTAATTTTATATACTGTAAGTTCCTGTG	4334	
Db	3366	TTGGCAATTTCAATTAAGGATTAATTTTATATACTGTAAGTTCCTGTG	3425	
Qy	4335	CTTATTTGGTTATGTTCCATCAGTTATCTGTTCACTTATATTTGCTTT	4394	
Db	3426	CTTATTTGGTTATGTTCCATCAGTTATCTGTTCACTTATATTTGCTTT	3485	
Qy	4395	AAAAATTTTAAATACCAAGAAATTTTGGTCAATTTTATCTATTTCTGT	4454	
Db	3486	AAAAATTTTAAATACCAAGAAATTTTGGTCAATTTTATCTATTTCTGT	3545	
Qy	4455	ATTGCAATCACTGAAATAAATCTTTTATTTGGGATACAAATTTGCAACT	4514	
Db	3546	ATTGCAATCACTGAAATAAATCTTTTATTTGGGATACAAATTTGCAACT	3605	
Qy	4515	GCCTTTTGTATCTCATCTCAATCTATCCATCTAGGTTGCCGTGATTTCT	4574	
Db	3606	GCCTTTTGTATCTCATCTCAATCTATCCATCTAGGTTGCCGTGATTTCT	3665	
Qy	4575	ATTTCTTGGAGAAATGCTAGGAAATGAGGACACCTATAATCCATGGGAT	4634	
Db	3666	ATTTCTTGGAGAAATGCTAGGAAATGAGGACACCTATAATCCATGGGAT	3725	
Qy	4635	GTAGCTGTTTATATCGCCTTACCTGCGAGTGTACTGTGGATTTTCTCTT	4694	

therapeutic, diagnostic and pharmacogenomic applications -

Disclosure; Page 45-46; 46pp; English.

XX The present sequence is a cDNA coding for novel human protein (NHP),
XX human transporter protein. NHPs shares structural similarity with
XX the mammalian ATP-binding cassette (ABC) transporters and multidrug
XX resistance transporters. NHP polynucleotides are useful for the
XX therapeutic, diagnostic and pharmacogenomic applications. They are
XX used for detecting and treating mental disorders and cancers. They
XX are also used in gene therapy. NHP polypeptides are useful for
XX diagnosis, drug screening, clinical trial monitoring, treatment of
XX diseases and disorders, and cosmetic or nutraceutical applications.
SQ Sequence 5262 BP; 1615 A; 888 C; 1012 G; 1743 T; 4 other;

Query Match 80.48; Score 5247.4; DB 24; Length 5262;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 5248; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy	757	ACTGTTGATATGGTGTATTTCAAATTCGTCTACCCCTATTTCCACATGCGCTTGTACT	816
Db	1	ACTGTTGATATGGTGTATTTCAAATTCGTCTACCCCTATTTCCACATGCGCTTGTACT	60
Qy	817	TTTCAGAGCTGACAGATGCTGCTCCATGCAATCTGCTCCAGTTTCTTAAGAGACAGCT	876
Db	61	TTTCAGAGCTGACAGATGCTGCTCCATGCAATCTGCTCCAGTTTCTTAAGAGACAGCT	120
Qy	877	TGGAGTATGCTTAATCATCTTACCTGGGACTGAAACAGCTGCTTATTTGCCGTTAAAA	936
Db	121	TGGAGTATGCTTAATCATCTTACCTGGGACTGAAACAGCTGCTTATTTGCCGTTAAAA	180
Qy	937	ATTACATGCAAGTTTACCTGCGTGGCTCCGGTGTGTTGTTGTTTCTCTTAAATAGG	996
Db	181	ATTACATGCAAGTTTACCTGCGTGGCTCCGGTGTGTTGTTGTTTCTCTTAAATAGG	240
Qy	997	TTTATTCCAGAAAACATGCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACGAA	1056
Db	241	TTTATTCCAGAAAACATGCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACGAA	300
Qy	1057	CACCTTCTACTGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1116
Db	301	CACCTTCTACTGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	360
Qy	1117	TTCTTTTCCACTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	1176
Db	361	TTCTTTTCCACTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	420
Qy	1177	AGAAATATGAAGAGTCCCTAATAGAACTCAATCCTATGGCAAGTTTACTTTCTA	1236
Db	421	AGAAATATGAAGAGTCCCTAATAGAACTCAATCCTATGGCAAGTTTACTTTCTA	480
Qy	1237	ATCTAATTTCTGGATATCTCCAGTGACTAATTAATTAATTAATTAATTAATTAATTAAT	1296
Db	481	ATCTAATTTCTGGATATCTCCAGTGACTAATTAATTAATTAATTAATTAATTAATTAAT	540
Qy	1297	CTACTGATCATCTACCTGATGTCATAATTAATTAATTAATTAATTAATTAATTAATTAAT	1356
Db	541	CTACTGATCATCTACCTGATGTCATAATTAATTAATTAATTAATTAATTAATTAATTAAT	600
Qy	1357	TAAACATCCAGTCTCTTAAGCCGAGCAACTTTGTAGGTGTGTTTCCAAAGACTCCATGT	1416
Db	601	TAAACATCCAGTCTCTTAAGCCGAGCAACTTTGTAGGTGTGTTTCCAAAGACTCCATGT	660
Qy	1417	CCTATGAACCTTGGTTTTTCTCGATATGATTCAGATCTCTTATTTATATGATTCAT	1476
Db	661	CCTATGAACCTTGGTTTTTCTCGATATGATTCAGATCTCTTATTTATATGATTCAT	720
Qy	1477	GAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGCTCAGGTTTCCACAGTTT	1536
Db	721	GAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGCTCAGGTTTCCACAGTTT	780
Qy	1537	TACAAGCATCCATAGATGCTGCCATTATACAGTTTGAAGACCAATGTTTCTTTTGGGAGG	1596

Db	781	TACAAGCATCCATAGATGCTGCCATTATATACAGTTGAAGACCAATGTTTCTTTTGAAGG	840
Qy	1597	AGCTTGAGTCAACTAAAGCTGTTTATTTATGCGAGAAACCTGCTGTGTAGAAATAGATACCT	1656
Db	841	AGCTTGAGTCAACTAAAGCTGTTTATTTATGCGAGAAACCTGCTGTGTAGAAATAGATACCT	900
Qy	1657	TTCCCGGAGAGTAAATTTTAAATATACCTAGTTATAGCATTTCACCTTTTGGTACTTTTT	1716
Db	901	TTCCCGGAGAGTAAATTTTAAATATACCTAGTTATAGCATTTCACCTTTTGGTACTTTTT	960
Qy	1717	TGCAATTCATATCGTAGCAGAAAAAGAAAAATAAAGAAATTTTAAAGATAATGG	1776
Db	961	TGCAATTCATATCGTAGCAGAAAAAGAAAAATAAAGAAATTTTAAAGATAATGG	1020
Qy	1777	GACTTCATGATGCTGCTTTTGGCTTTCTCTGGGTCTCTCTATATACAAAGTTTAAATTTTC	1836
Db	1021	GACTTCATGATGCTGCTTTTGGCTTTCTCTGGGTCTCTCTATATACAAAGTTTAAATTTTC	1080
Qy	1837	TTATGTCCTTCTTATGGCAGTCATTGCGACAGCTTCTTTGTTTATTTCTCAAAGTAGCA	1896
Db	1081	TTATGTCCTTCTTATGGCAGTCATTGCGACAGCTTCTTTGTTTATTTCTCAAAGTAGCA	1140
Qy	1897	GCATTTGATATTTCTGCTTTTCTTATGGAATTAATCTGTAATTTTTCCTTTAA	1956
Db	1141	GCATTTGATATTTCTGCTTTTCTTATGGAATTAATCTGTAATTTTTCCTTTAA	1200
Qy	1957	TGCTGACACCTCTTTTAAATAATCAAAATGCGGAAATAGTTGAATTTTGTACTG	2016
Db	1201	TGCTGACACCTCTTTTAAATAATCAAAATGCGGAAATAGTTGAATTTTGTACTG	1260
Qy	2017	TGCTTTTGGATTTATGTCCTTATGATTAATCTCATAGAAAGTTTCCAAATCGTTAG	2076
Db	1261	TGCTTTTGGATTTATGTCCTTATGATTAATCTCATAGAAAGTTTCCAAATCGTTAG	1320
Qy	2077	TGCGCTTTTCACTCTTCTGTCACCTTTTGTGATTTGATTTGCAAGGTCAAGC	2136
Db	1321	TGCGCTTTTCACTCTTCTGTCACCTTTTGTGATTTGATTTGCAAGGTCAAGC	1380
Qy	2137	ATTAGAAGATTTTAAATGAGGTGCTTCAATTTTGAAGTGGAGTGGAGTGGAGTGGAGT	2196
Db	1381	ATTAGAAGATTTTAAATGAGGTGCTTCAATTTTGAAGTGGAGTGGAGTGGAGTGGAGT	1440
Qy	2197	TAATTAATCAATTAATCATGCTCACACTTAATAGTATATTTCTATGCTCTTGGCTGCT	2256
Db	1441	TAATTAATCAATTAATCATGCTCACACTTAATAGTATATTTCTATGCTCTTGGCTGCT	1500
Qy	2257	ATCTTGATCAAGTCAATTCAGGGGAAATTTGGCTTACGGAGATCATCTTTATATTTCTGA	2316
Db	1501	ATCTTGATCAAGTCAATTCAGGGGAAATTTGGCTTACGGAGATCATCTTTATATTTCTGA	1560
Qy	2317	AGCTTTTATATGCTCAAGAGTAAAGAAATTTATGAGGATTTATCAGAGGCAATGTTA	2376
Db	1561	AGCTTTTATATGCTCAAGAGTAAAGAAATTTATGAGGATTTATCAGAGGCAATGTTA	1620
Qy	2377	ATGGAATATTTAGTTTATGAGGAGTAAAGAAATTTATGAGGATTTATCAGAGGCAATGTTA	2436
Db	1621	ATGGAATATTTAGTTTATGAGGAGTAAAGAAATTTATGAGGATTTATCAGAGGCAATGTTA	1680
Qy	2437	AGCCATAAGAAATTTAGTGGTATTCAGAGACATACAGAGAGGAGGTTGAAATTTGGAGG	2496
Db	1681	AGCCATAAGAAATTTAGTGGTATTCAGAGACATACAGAGAGGAGGTTGAAATTTGGAGG	1740
Qy	2497	CTTTGAGAAATTTGCTATTTGACATATATGAGGCTCAGATTACTGCTTACTTTGGCCACA	2556
Db	1741	CTTTGAGAAATTTGCTATTTGACATATATGAGGCTCAGATTACTGCTTACTTTGGCCACA	1800
Qy	2557	GTGGAACAGAAAGAGTACATTTGATCAATATTTCTTTGTGAGCTCTGCCACCTTCTGATG	2616
Db	1801	GTGGAACAGAAAGAGTACATTTGATCAATATTTCTTTGTGAGCTCTGCCACCTTCTGATG	1860
Qy	2617	GGTTTGCATCTATATATGAGACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAA	2676

1861 GGTTTGCACTATATATGAGACAGAGCTCTCAGAAATAGATGAAATGTTTGAAGCAAGAA 1920
Qy
2677 AAATGATGCGAATTTGTCACAGCTAGATATACTTTGATGTTTGAAGTAGAAGAA 2736
Db
1921 AAATGATGCGAATTTGTCACAGCTAGATATACTTTGATGTTTGAAGTAGAAGAA 1980
Qy
2737 ATTTATCAATTTTGGCTTCAATCAAGGGATACAGCCCAACATAATAATACAGAAAGTGC 2796
Db
1981 ATTTATCAATTTTGGCTTCAATCAAGGGATACAGCCCAACATAATAATACAGAAAGTGC 2040
Qy
2797 AGAAGGTTTTACTAGATTTAGACATGACAGACTATCAAGATATCAAGATATCAAGATATCA 2856
Db
2041 AGAAGGTTTTACTAGATTTAGACATGACAGACTATCAAGATATCAAGATATCAAGATATCA 2100
Qy
2857 GTGGTGTCAAAAAGAAAGCTGTCAATAGGAATGCTGTCTTGGGAACCCCAAGATAC 2916
Db
2101 GTGGTGTCAAAAAGAAAGCTGTCAATAGGAATGCTGTCTTGGGAACCCCAAGATAC 2160
Qy
2917 TGCTGCTAGATGAACCAAGCTGGAAATGACCCCTGTTCTCGACATATTTGATGGAATC 2976
Db
2161 TGCTGCTAGATGAACCAAGCTGGAAATGACCCCTGTTCTCGACATATTTGATGGAATC 2220
Qy
2977 TTTTAAATACAGAAAGCCAAATCGGGTGAAGCTTTAGTATCAATTTCAATGATGAAG 3036
Db
2221 TTTTAAATACAGAAAGCCAAATCGGGTGAAGCTTTAGTATCAATTTCAATGATGAAG 2280
Qy
3037 CTGACATTTCTGCAGATAGAAAGCTGTGATATCAAGAAATGCTGGAATGTTGGTT 3096
Db
2281 CTGACATTTCTGCAGATAGAAAGCTGTGATATCAAGAAATGCTGGAATGTTGGTT 2340
Qy
3097 CTTCAATGTTCTTCAAAAGTAATGGGGATCGGCTACCCCTGAGCATGTACATAGACA 3156
Db
2341 CTTCAATGTTCTTCAAAAGTAATGGGGATCGGCTACCCCTGAGCATGTACATAGACA 2400
Qy
3157 AATATTGTCGACAGAAATCTCTTTCTTCACTGGTTAAACAAATATACCTGGAGCTACTT 3216
Db
2401 AATATTGTCGACAGAAATCTCTTTCTTCACTGGTTAAACAAATATACCTGGAGCTACTT 2460
Qy
3217 TATTAAACAGATGACCAACACTTGTGTATAGCTTGCCTTTCAAGGACATGGCAAAAT 3276
Db
2461 TATTAAACAGATGACCAACACTTGTGTATAGCTTGCCTTTCAAGGACATGGCAAAAT 2520
Qy
3277 TTTTCAGGTTTGTCTTGCCTTAGACATCAATCAAAATTTGGGTGTCTTCTTATGGTG 3336
Db
2521 TTTTCAGGTTTGTCTTGCCTTAGACATCAATCAAAATTTGGGTGTCTTCTTATGGGG 2580
Qy
3337 TTTTCATGACGACTTTTGGAAAGAGCTATTTTTAAAGCTAGAAAGTTGAAGCAGAAATGACC 3396
Db
2581 TTTTCATGACGACTTTTGGAAAGAGCTATTTTTAAAGCTAGAAAGTTGAAGCAGAAATGACC 2640
Qy
3397 AAGCAGATTTATGTATTTACTCAGCAGCCACTGGAGGAAAGAAATGGATTCAAAATCTT 3456
Db
2641 AAGCAGATTTATGTATTTACTCAGCAGCCACTGGAGGAAAGAAATGGATTCAAAATCTT 2700
Qy
3457 TTGATGAATTTGGAACACAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGAGCA 3516
Db
2701 TTGATGAATTTGGAACACAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGAGCA 2760
Qy
3517 CCATGAGCCTTTTGGAAACAAACAGATGATACATAGCAAAAGTTTCAATTTCTTACCTTGA 3576
Db
2761 CCATGAGCCTTTTGGAAACAAACAGATGATACATAGCAAAAGTTTCAATTTCTTACCTTGA 2820
Qy
3577 AACGTGAAGTAATCAGTGAGATCAGTGTTGCTTCTGCTTTTAAATTTTTTTCACAGTTC 3636
Db
2821 AACGTGAAGTAATCAGTGAGATCAGTGTTGCTTCTGCTTTTAAATTTTTTTCACAGTTC 2880
Qy
3637 AGATTTTTTATGTTTTTGGTTTCATCAGCTCTTTTAAATGCTGTGGTTTCCCATCAAACTTG 3696
Db
2881 AGATTTTTTATGTTTTTGGTTTCATCAGCTCTTTTAAATGCTGTGGTTTCCCATCAAACTTG 2940
Qy
3697 TTCCAGACTTATATTTTCTAAACCTGGAGACAAACACATAAATAACAAACAAAGTCTGC 3756
Db
2941 TTCCAGACTTATATTTTCTAAACCTGGAGACAAACACATAAATAACAAACAAAGTCTGC 3000

3757 TTCTTCAAAATTTCTGCTGACTCAGATATCAGTGATCTTTATTAGCTTTTTTCAAGCCAGA 3816
Qy
3001 TTCTTCAAAATTTCTGCTGACTCAGATATCAGTGATCTTTATTAGCTTTTTCAAGCCAGA 3060
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3817 ACATAATCGTGACGATGATTAATGACAGTGACTATGATATCGGTGGCTCCCATAGTGGG 3876
Qy
3061 ACATAATCGTGACGATGATTAATGACAGTGACTATGATATCGGTGGCTCCCATAGTGGG 3120
Db
3877 CTTTAAATGTCATGCAATTCAGAAAGGACTATGTTTTTGCAGCTGTTTTCAACACTATA 3936
Qy
3121 CTTTAAATGTCATGCAATTCAGAAAGGACTATGTTTTTGCAGCTGTTTTCAACACTATA 3180
Db
3937 TGGTTTATTTCTTACTATATTAGTGAATATCAATTAGTAACTACTATCTTTTATCATTTAA 3996
Qy
3181 TGGTTTATTTCTTACTATATTAGTGAATATCAATTAGTAACTACTATCTTTTATCATTTAA 3240
Db
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Qy
3241 ATGTGACTGAAACCAATCCAGATCTGGAGTACCCCACTCTTTCAAGAAATTAATGATATAG 3300
Db
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Qy
3301 TTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCAATGCTGCAATGC 3360
Db
4117 CACCTTTACTTTGCCATGGAATAATGAGAGATCAATAGATCAAAAGCTTTATATCAACTTA 4176
Qy
3361 CACCTTTACTTTGCCATGGAATAATGAGAGATCAATAGATCAAAAGCTTTATATCAACTTA 3420
Db
4177 AACTTTCAAGCTTTTGGCATCTGCAATATGGATGGACAAAGCTGTTGTTGATATCCCT 4236
Qy
3421 AACTTTCAAGCTTTTGGCATCTGCAATATGGATGGACAAAGCTGTTGTTGATATCCCT 3480
Db
4237 TATTTTATCACTTCTTATTTTGTAGCTAGAGCTTACTGCAATTCATTTATGATGATAT 4296
Qy
3481 TATTTTATCACTTCTTATTTTGTAGCTAGAGCTTATTTGCAATTTCAATTTATGATGATAT 3540
Db
4297 ATTTTATCACTTCTTATTTTGTAGCTAGAGCTTATTTGCAATTTCAATTTATGATGATAT 4356
Qy
3541 ATTTTATCACTTCTTATTTTGTAGCTAGAGCTTATTTGCAATTTCAATTTATGATGATAT 3600
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4357 TATTTCTGTTCACTTATATATGCTTCTTTCACTTTTAAAGAAATTTTAAATACCAAGAT 4416
Qy
3601 TATTTCTGTTCACTTATATATGCTTCTTTCACTTTTAAAGAAATTTTAAATACCAAGAT 3660
Db
4417 TTTGTCATTTATCTTATTTCTGTCGAGCTGTTGCTTGTATTTGCAATCTAGTAAATCTT 4476
Qy
3661 TTTGTCATTTATCTTATTTCTGTCGAGCTGTTGGCTTGTATTTGCAATCTAGTAAATCTT 3720
Db
4477 TCTTTATGCGATACACAATTTGCAACTTATTTCTTATGTCCTTTTGTATCATTTCCAA 4536
Qy
3721 TCTTTATGCGATACACAATTTGCAACTTATTTCTTATGTCCTTTTGTATCATTTCCAA 3780
Db
4537 TCTATCCACTTCTAGTTGCTGATTTCTTTTCAATAAAGATTTCTTTGGAAGAAATGACGAA 4596
Qy
3781 TCTATCCACTTCTAGTTGCTGATTTCTTTTCAATAAAGATTTCTTTGGAAGAAATGACGAA 3840
Db
4597 AAAATGTGACACCTTATTAATCCATGGGATAGGCTTTGATAGCTGTTTATATCGCTTACC 4656
Qy
3841 AAAATGTGACACCTTATTAATCCATGGGATAGGCTTTGATAGCTGTTTATATCGCTTACC 3900
Db
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Qy
3901 TGCAGTGTGATCTGCGAATTTTCTTCAATATCTATGAGAAATAATATGAGGCGAGAT 3960
Db
4717 CAATAAGAAAGATCCCTTTTTCAGAAAACCTTTTCAACGAAGCTTAAATAATAGAAAGCTTC 4776
Qy
3961 CAATAAGAAAGATCCCTTTTTCAGAAAACCTTTTCAACGAAGCTTAAATAATAGAAAGCTTC 4020
Db
4777 CAGAAACCAACAGCAANTCAGGATGAAGATGAAGATGTCAAAGCTTAAAGACTTAAAGGTCA 4836
Qy
4021 CAGAAACCAACAGCAANTCAGGATGAAGATGAAGATGTCAAAGCTTAAAGACTTAAAGGTCA 4080
Db

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Qy 4837 AAGAGCTGATGGGTGCGAGTGTGTGAGGAGAAACCATCATATATGCTCAGCAATTTGC 4896
Db 4081 AAGAGCTGATGGGTGCGAGTGTGTGAGGAGAAACCATCATATGCTCAGCAATTTGC 4140
Qy 4897 ATAAGAATATGATGACAAGAGATTTCTCTTTCAAGAAAGTAAAGAAAGTGGCAA 4956
Db 4141 ATAAGAATATGATGACAAGAGATTTCTCTTTCAAGAAAGTAAAGAAAGTGGCAA 4200
Qy 4957 CTAATATCATCTCTTTCTGTGTGAAAAAGAGAGATCTTTAGGACTATTTGGTCCAAATG 5016
Db 4201 CTAATATCATCTCTTTCTGTGTGAAAAAGAGAGATCTTTAGGACTATTTGGTCCAAATG 4260
Qy 5017 GTGCTGCAAAAGACAAATATTAATATTTCTGTTGGTGTGATATTAAGAACCACTTCAGGCC 5076
Db 4261 GTGCTGCAAAAGACAAATATTAATATTTCTGTTGGTGTGATATTAAGAACCACTTCAGGCC 4320
Qy 5077 AGGTATTTTGGAGATATTTCTTCAGAGACAGTGAAGATGATGATTCACCTCAAGTGTA 5136
Db 4321 AGGTATTTTGGAGATATTTCTTCAGAGACAGTGAAGATGATGATTCACCTCAAGTGTA 4380
Qy 5137 TGGGTACTGTCTTCAGATAAACCCCTTTGTGGCCAGATACATTCAGAGAAACATTTTG 5196
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Db 4981 TTCAGTCCCTTTCACAACTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGGCAATG 5040
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Qy 5857 AAGAGGAGGAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGTGGGAGACGACAC 5916
Db 5101 AAGAGGAGGAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGTGGGAGACGACAC 5160
Qy 5917 AAGAGATAGAGTAGTATTTTGAATTTGTATTTGTTGCTGCTGCTTACTGGGACTTCTTTC 5976
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Db 5161 AAGAAGATAGATAGTATTTTGAATTTGATTTGCTGCTGCTTACTGGGACTTCTTTC 5220
Qy 5977 TTTTTCACCTTAATTTTAACTTTGTTGTTTAAAAAGTTTTT 6014
Db 5221 TTTTTCACCTTAATTTTAACTTTGTTGTTTAAAAAGTTTTT 5258

RESULT 6
AAD37618
ID AAD37618 standard; cDNA; 4929 BP.
XX
AC AAD37618;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human transporter protein cDNA #1.
XX
KW Human; novel human protein; NHP; transporter protein; mental disorder;
KW cancer; gene therapy; drug screening; nutraceutical application; gene;
KW cosmetic application; polymorphism; ss.
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Key Location/Qualifiers
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FT misc_feature 2878
FT /*tag= d
FT /note= "This degenerate base represents a
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WO200231147-A2.
XX
PD 18-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US311113.
XX
PR 10-OCT-2000; 2000US-239629P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Nepomnichy B;
XX
DR WPI: 2002-452347/48.
XX P-PSDB; AAE23656.
XX
FT Novel nucleic acid molecule encoding novel human proteins, useful for
FT therapeutic, diagnostic and pharmacogenomic applications -
XX
PS Claim 1; Page 34-35; 46pp; English.
XX
CC The present sequence is a cDNA coding for novel human protein (NHP),
CC human transporter protein. NHPs shares structural similarity with
CC the mammalian ATP-binding cassette (ABC) transporters and multidrug
CC resistance transporters. NHP polynucleotides are useful for the
CC therapeutic, diagnostic and pharmacogenomic applications. They are
CC used for detecting and treating mental disorders and cancers. They
CC are also used in gene therapy. NHP polypeptides are useful for
CC diagnosis, drug screening, clinical trial monitoring, treatment of
CC diseases and disorders, and cosmetic or nutraceutical applications.
CC
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XX	Sequence	4929 BP; 1544 A; 827 C; 950 G; 1604 T; 4 other;	
SQ	Query Match	75.4%; Score 4918.4; DB 24; Length 4929;	
	Best Local Similarity	99.8%; Pred. No. 0;	
	Matches 4919; Conservative	4; Mismatches 6; Indels 0; Gaps 0;	
Qy	1011	ATGTCCTCACTGCAATTTAGGGAGGTAGGAGTTTGGAGACAGACCAAGACACTTCTACTGAAG	1070
Db	1	ATGTCCTCACTGCAATTTAGGGAGGTAGGAGTTTGGAGACAGACCAAGACACTTCTACTGAAG	60
Qy	1071	AATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTA	1130
Db	61	AATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTA	120
Qy	1131	TTTTTTTTTATTTGGTTAAATTAATAGCATGATGCATCCAAATAAGAAATATGAAGAA	1190
Db	121	TTTTTTTTTATTTGGTTAAATTAATAGCATGATGCATCCAAATAAGAAATATGAAGAA	180
Qy	1191	GTGCTAATATAGAACTCAATCTATGACAAAGTTTACTCTTTCTAATCTAAATTTCTTGA	1250
Db	181	GTGCTAATATAGAACTCAATCTATGACAAAGTTTACTCTTTCTAATCTAAATTTCTTGA	240
Qy	1251	TATACTCCAGTGACTAATATTTACAAGCAGCATCATGCGAGAAAGTGCTACTGATCATCTA	1310
Db	241	TATACTCCAGTGACTAATATTTACAAGCAGCATCATGCGAGAAAGTGCTACTGATCATCTA	300
Qy	1311	CTGATGCTAATTAATCTGAAGAAATATACAAATGAAAGAAATGTTAAATCAAGTCTC	1370
Db	301	CTGATGCTAATTAATTAATCTGAAGAAATATACAAATGAAAGAAATGTTAAATCAAGTCTC	360
Qy	1371	TCTAAGCCGAGCACTTTGTAGGTGCTTTTCAAGACTCCATGCTCTATGAATTCGT	1430
Db	361	TCTAAGCCGAGCACTTTGTAGGTGCTTTTCAAGACTCCATGCTCTATGAATTCGT	420
Qy	1431	TTTTTTCTGATATGATTCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTCTA	1490
Db	421	TTTTTTCTGATATGATTCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTCTA	480
Qy	1491	AAATCATGTGAGGCTGCTAGTACTGTGCTCAGGTTTCACAGTTTACAGCATCCATA	1550
Db	481	AAATCATGTGAGGCTGCTAGTACTGTGCTCAGGTTTTCACAGTTTACAGCATCCATA	540
Qy	1551	GATGCTGCCATTATACAGTTTGAAGCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT	1610
Db	541	GATGCTGCCATTATACAGTTTGAAGCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT	600
Qy	1611	AAAGCTGTTATTTAGGAGAACTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTA	1670
Db	601	AAAGCTGTTATTTAGGAGAACTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTA	660
Qy	1671	ATTTTAATATACCTAGTTATAGATTTTACCTTTTGGATACCTTTTGGCAATTCATATC	1730
Db	661	ATTTTAATATACCTAGTTATAGATTTTACCTTTTGGATACCTTTTGGCAATTCATATC	720
Qy	1731	GTACGAGAAAGAGAAATAAAGAAATTTTAAAGATAATGGACACTTCATGATACT	1790
Db	721	GTACGAGAAAGAGAAATAAAGAAATTTTAAAGATAATGGACACTTCATGATACT	780
Qy	1791	GCCTTTTGGCTTCTCCTGGGTTCTTCTATATACAGTTTAAATTTTCTATGTCCTCTTT	1850
Db	781	GCCTTTTGGCTTCTCCTGGGTTCTTCTATATACAGTTTAAATTTTCTATGTCCTCTTT	840
Qy	1851	ATGCGAGTCAATGGGACAGCTTCTTTGTTATTTCTCCTCAAGATAGCAGCATTTGATATTT	1910
Db	841	ATGCGAGTCAATGGGACAGCTTCTTTGTTATTTCTCCTCAAGATAGCAGCATTTGATATTT	900
Qy	1911	CTGCTTTTTTCTTTTATGATATCATCTGATTTTTTCTTTTAAAGCTGACACTCTTT	1970
Db	901	CTGCTTTTTTCTTTTATGATATCATCTGATTTTTTCTTTTAAAGCTGACACTCTTT	960
Qy	1971	TTTTAAAAAATCAAAACATGTGGGAATAGTTCATTTTTTTGTTACTGTGGCTTTTGGATTT	2030

Db	961	TTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTTTTGTACTGTGGCTTTTGGATTT	1020
Qy	2031	ATTGGCTTATGATATATCTCTCATAGAAAGTTTTTCCCAAATCGTTAGTGTGGCTTTTCACT	2090
Db	1021	ATTGGCTTATGATATATCTCTCATAGAAAGTTTTTCCCAAATCGTTAGTGTGGCTTTTCACT	1080
Qy	2091	CCTTTCTGTCACTGTACTTTTGTGATTTGTCACAGGTCAATGATTTAGAGAATTTT	2150
Db	1081	CCTTTCTGTCACTGTACTTTTGTGATTTGTCACAGGTCAATGATTTAGAGAATTTT	1140
Qy	2151	AATGAAGGTGCTTCAATTTTCAAAATTTGACTGAGGCCCATATCTCTTAATTAATTAATTT	2210
Db	1141	AATGAAGGTGCTTCAATTTTCAAAATTTGACTGAGGCCCATATCTCTTAATTAATTAATTT	1200
Qy	2211	ATCATGCTCACACTTAATAGTATATTTCTATGTCCTTGGCTGTCTATCTGATCAAGTC	2270
Db	1201	ATCATGCTCACACTTAATAGTATATTTCTATGTCCTTGGCTGTCTATCTGATCAAGTC	1260
Qy	2271	ATTCCAGGGGAATTTGGCTTTACGGAGATCATCTTTATATTTTCTGAAGCTTTCATATGG	2330
Db	1261	ATTCCAGGGGAATTTGGCTTTACGGAGATCATCTTTATATTTTCTGAAGCTTTCATATGG	1320
Qy	2331	TCAAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGAATATTAAGT	2390
Db	1321	TCAAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGAATATTAAGT	1380
Qy	2391	TTTAGTGAATTTATTTGAGCCAGTTTCTCAGAAATTTGTAGGAAAGAAAGCCATAAGAAAT	2450
Db	1381	TTTAGTGAATTTATTTGAGCCAGTTTCTCAGAAATTTGTAGGAAAGAAAGCCATAAGAAAT	1440
Qy	2451	AGTGGTATTTCAGAGACATACAGAAAGAGGTGAAAATTTGTGAGGCTTTTGAGAAATTTTG	2510
Db	1441	AGTGGTATTTCAGAGACATACAGAAAGAGGTGAAAATTTGTGAGGCTTTTGAGAAATTTTG	1500
Qy	2511	TCATTTGACATATATGAGGCTCAGATTACTGCTTACTTTGGCCACAGTGGAAACAGAGAAAG	2570
Db	1501	TCATTTGACATATATGAGGCTCAGATTACTGCTTACTTTGGCCACAGTGGAAACAGAGAAAG	1560
Qy	2571	AGTACATTGATCAATATTTTGTGAGCTCTCCGACCTTCTGATGGGTTTGCATCTATA	2630
Db	1561	AGTACATTGATCAATATTTTGTGAGCTCTCCGACCTTCTGATGGGTTTGCATCTATA	1620
Qy	2631	TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAATAATGATGSCATT	2690
Db	1621	TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAATAATGATGSCATT	1680
Qy	2691	TGTCCACAGTTAGATATACACTTTGATGTTTGAAGTAAAGAAATAATTTATCAATTTTG	2750
Db	1681	TGTCCACAGTTAGATATACACTTTGATGTTTGAAGTAAAGAAATAATTTATCAATTTTG	1740
Qy	2751	GCTTCAATCAAGGGATACCGCCCAATATAATACAGAAAGTGCAGAAAGTTTFACTA	2810
Db	1741	GCTTCAATCAAGGGATACCGCCCAATATAATACAGAAAGTGCAGAAAGTTTFACTA	1800
Qy	2811	GATTTAGACATCGAGATATCAAGATACCAAGCTAAAAAATAAGTGGTGGTCAAAAA	2870
Db	1801	GATTTAGACATCGAGATATCAAGATACCAAGCTAAAAAATAAGTGGTGGTCAAAAA	1860
Qy	2871	AGAAAGCTGTCAATAGGAATTCCTGTTTGGGAACCCCAAGATACCTGCTGATAGTAA	2930
Db	1861	AGAAAGCTGTCAATAGGAATTCCTGTTTGGGAACCCCAAGATACCTGCTGATAGTAA	1920
Qy	2931	CCAAAGCTGGAATGGACCCCTGTTCTGACATATTTGATGAAATCTTTTAAAAATACAGA	2990
Db	1921	CCAAAGCTGGAATGGACCCCTGTTCTGACATATTTGATGAAATCTTTTAAAAATACAGA	1980
Qy	2991	AAAGCAATCGGGTGCAGTGTTCAGTACTCAATTTTCATGATGAAAGCTGACATTTCTTGA	3050
Db	1981	AAAGCAATCGGGTGCAGTGTTCAGTACTCAATTTTCATGATGAAAGCTGACATTTCTTGA	2040
Qy	3051	GATAGAAAGCTGTGATATCAAGAAATGCTGAAATGTGTTGGTTCCTCAATGTCTCTC	3110
Db	2041	GATAGAAAGCTGTGATATCAAGAAATGCTGAAATGTGTTGGTTCCTCAATGTCTCTC	2100

QY	3111	AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA	3170
DB	2101	AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA	2160
QY	3171	GAATCTCTTTCTTCACCTGGTTAAACAACATATACCTGGAGCTACTTTATTAACAAGAAAT	3230
DB	2161	GAATCTCTTTCTTCACCTGGTTAAACAACATATACCTGGAGCTACTTTATTAACAAGAAAT	2220
QY	3231	GACCAACAACTGTGTATAGCTTCCCTTCAAGGACATGACAAATTTTCAGGTGTGTTT	3290
DB	2221	GACCAACAACTGTGTATAGCTTCCCTTCAAGGACATGACAAATTTTCAGGTGTGTTT	2280
QY	3291	TCTGCCCTTAGACAGCTCAATCAAAATTTGGGTGTCAATTTCTTATGGTGTTCATGACGACT	3350
DB	2281	TCTGCCCTTAGACAGCTCAATCAAAATTTGGGTGGCAATTTCTTATGGGTTCATGACGACT	2340
QY	3351	TTGGAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAGAAATTTGACCAAGCAGATTAAGT	3410
DB	2341	TTGGAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAGAAATTTGACCAAGCAGATTAAGT	2400
QY	3411	GTATTTTACTCAGCAGCAGCTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAATGGAA	3470
DB	2401	GTATTTTACTCAGCAGCAGCTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAATGGAA	2460
QY	3471	CAGAGCTTACTTATCTTTCTGAAACCAAGCTTCTCTAGTGAGCACCATTGAGCCTTTGG	3530
DB	2461	CAGAGCTTACTTATCTTTCTGAAACCAAGCTTCTCTAGTGAGCACCATTGAGCCTTTGG	2520
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DB	2521	AAACAACAGATGATACAAATAGCAAAAGTTTCATTTCTTTTACCTTGAAACGTTGAAAGTAA	2580
QY	3591	TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT	3650
DB	2581	TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT	2640
QY	3651	TTGGTTTCACTCACTTTTAAATATGCTGTGTTTCCCATCAAACTTGTTCAGAGCTTATAT	3710
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QY	3771	GCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAGCCAGACATAAATGGTGACG	3830
DB	2761	GCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAGCCAGACATAAATGGTGACG	2820
QY	3831	ATGATTAATGACAGTGAATGTATCGTGGCTCCCATAGTGGGCTTTTAAATGTGATG	3890
DB	2821	ATGATTAATGACAGTGAATGTATCGTGGCTCCCATAGTGGGCTTTTAAATGTGATG	2880
QY	3891	CATTGAGAAAAGGACTATGTTTGTGAGCTGTTTTCACAGTACTATGTTTATCTTTTA	3950
DB	2881	CATTGAGAAAAGGACTATGTTTGTGAGCTGTTTTCACAGTACTATGTTTATCTTTTA	2940
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DB	2941	CTTATATAGTGAATATCATTAGTAATCTATCTTTTATCATTTAATGTGACTGAAACC	3000
QY	4011	ATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTAATGATATAGTTTAAATTTGAG	4070
DB	3001	ATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTAATGATATAGTTTAAATTTGAG	3060
QY	4071	CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTAATGCAATGCCACCTTACTTTGCC	4130
DB	3061	CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTAATGCAATGCCACCTTACTTTGCC	3120
QY	4131	ATGGAATGAGAGAAATCATAGATCAAGCTTTATCTCAACTTAACTTCAGGTCTTT	4190
DB	3121	ATGGAATGAGAGAAATCATAGATCAAGCTTTATCTCAACTTAACTTCAGGTCTTT	3180

QY	4191	TTGCCATCTGCATPATTTGGATTGGCAAGCTGTTGTTGATATCCCTTATTTTATCATTT	4250
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DB	3241	CTTATTTTGTATGCTAGGAAGCTTATTGGGCATTTTCATATGGATATATTTTATCTGTA	3300
QY	4311	AAGTCTCTTGTCTGTGTTTTCCTTATTTGGTTATGTTTCCATCAGTATTTCTGTTTCACT	4370
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QY	4371	TATATTGCTTCTTTTACCTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCAATTTATC	4430
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DB	3421	TATTTCTGGCAGCGTTGCTTGTATTTGCAATCACTGAAATTAATCTTTCTTTATGGGATAC	3480
QY	4491	ACAAATGCAACTATTTCTTCAATATGCTTTTGTATCATCTCAATCTATCCACTTTCTA	4550
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QY	4551	GGTTGCTGATTTCTTTTCAATAAGATTTCTTGAAGAAATGTCGAAAAATTTGGACACC	4610
DB	3541	GGTTGCTGATTTCTTTTCAATAAGATTTCTTGAAGAAATGTCGAAAAATTTGGACACC	3600
QY	4611	TATAATCCATGGGATAGGCTTTTTCAGTAGCTGTTTATATGCGCTTACCTGCGAGTGTACTG	4670
DB	3601	TATAATCCATGGGATAGGCTTTTTCAGTAGCTGTTTATATGCGCTTACCTGCGAGTGTACTG	3660
QY	4671	TGGATTTTCTCTTACAATACTATGAGAAAAATATGGAGGAGAGATCAATAAGAAAGAT	4730
DB	3661	TGGATTTTCTCTTACAATACTATGAGAAAAATATGGAGGAGAGATCAATAAGAAAGAT	3720
QY	4731	CCCTTTTTCAGAAACCTTTTCAACGAAGCTTAAATAAGAGCTTCCAGAACCCAGAC	4790
DB	3721	CCCTTTTTCAGAAACCTTTTCAACGAAGCTTAAATAAGAGCTTCCAGAACCCAGAC	3780
QY	4791	AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTTAAAGGTCAAAGCTGATGGGT	4850
DB	3781	AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTTAAAGGTCAAAGCTGATGGGT	3840
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DB	3841	TGCGAGTGTGTGAGGAGAAACCATCCATTTATGCTCAGCAATTTTGCATTAAGATATGAT	3900
QY	4911	GACAAGAAAGATTTTCTTTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCT	4970
DB	3901	GACAAGAAAGATTTTCTTTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCT	3960
QY	4971	TTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTTGGTCCAAATGGTGTGCGCAAAAGC	5030
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QY	5031	ACAAATTTAATATCTGTTGTTGATATTTGACCAACTTTCAGGCCAGGTATTTTATGGA	5090
DB	4021	ACAAATTTAATATCTGTTGTTGATATTTGACCAACTTTCAGGCCAGGTATTTTATGGA	4080
QY	5091	GATTATTTCTTCAGAGCAAGTGAAGATGATTTTCACTGAAGTGTATGGGTACTGTCTCT	5150
DB	4081	GATTATTTCTTCAGAGCAAGTGAAGATGATTTTCACTGAAGTGTATGGGTACTGTCTCT	4140
QY	5151	CAGATAAACCTTTTGTGGCCAGATCTACATTCAGGAAACATTTTGAAATTTATGGAGCT	5210
DB	4141	CAGATAAACCTTTTGTGGCCAGATCTACATTCAGGAAACATTTTGAAATTTATGGAGCT	4200
QY	5211	GTCAAAGGAATGAGTGCAGTGAATGAAGAGATCATAGTGCATTAACACATGCACTT	5270
DB	4201	GTCAAAGGAATGAGTGCAGTGAATGAAGAGATCATAGTGCATTAACACATGCACTT	4260
QY	5271	GATTTTAAAGAAACATCTTTCAGAGAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAG	5330

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DB	301	CCTGATGTCATAATTA	360
QY	1371	TCTAAGCCGAGCAACT	1430
DB	361	TCTAAGCCGAGCAACT	420
QY	1431	TTTTTTTCCGATAGAT	1490
DB	421	TTTTTTTCCGATAGAT	480
QY	1491	AAATCATGTGAGGCTG	1550
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QY	1551	GATGCTGCCATTAATA	1610
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QY	1611	AAAGCTGTTATATGG	1670
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QY	1731	GTAGCAGAAAAGAAA	1790
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QY	1791	GCCTTTTGGCTTTCCT	1850
DB	781	GCCTTTTGGCTTTCCT	840
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DB	841	ATGCGAGTCATGCGA	900
QY	1911	CTGCTTTTTCCTTTAT	1970
DB	901	CTGCTTTTTCCTTTAT	960
QY	1971	TTTTAAAAATCAAACA	2030
DB	961	TTTTAAAAATCAAACA	1020
QY	2031	ATTGGCCTTATGATAA	2090
DB	1021	ATTGGCCTTATGATAA	1080
QY	2091	CCTTTCTGTCACTGTA	2150
DB	1081	CCTTTCTGTCACTGTA	1140
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QY	2331	TCAAAGAGTAAAGAAA	2390
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QY	2391	TTTAGTGAATAATTAAT	2450
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DB	1681	TGTCCACAGTTAGATAT	1740
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DB	1741	GCTTCAATCAAAAGGG	1800
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QY	2931	CCAAACAGCTGGAAAT	2990
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DB	1981	AAAGCCAAATCGGGTG	2040
QY	3051	GATAGGAAGCTGTGAT	3110
DB	2041	GATAGGAAGCTGTGAT	2100
QY	3111	AAAAAGTAAATGGGGG	3170
DB	2101	AAAAAGTAAATGGGGG	2160
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DB	2161	GAATCTCTTTTCACTG	2220
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DB	2221	GACCAACAACTTGTGT	2280
QY	3291	TCTGCCCTTAGACAGT	3350
DB	2281	TCTGCCCTTAGACAGT	2340
QY	3351	TTGGAAAGAGCTATTT	3410
DB	2341	TTGGAAAGAGCTATTT	2400
QY	3411	GTATTTTACTCAGCAG	3470
DB	2401	GTATTTTACTCAGCAG	2460
QY	3471	CAGAGCTTACTTATTT	3530


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QY 5672 CCAGATGCAAGCGTCAGGAAAGTTTCTTCTATTTTGGCTTATATAATTCCTAAGGA 5731
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QY 5732 AGATGTCAGTCCTTTCACAACTTTTAAAGCTGGAAGAGCTTAAACATGCTTTTGC 5791
DB 4710 AGATGTCAGTCCTTTCACAACTTTTAAAGCTGGAAGAGCTTAAACATGCTTTTGC 4769
QY 5792 CATTGAAGATATAGCTTTCTCAAGCAACATTGGACAGCTTTTCTAGAAGCTCACTAA 5851
DB 4770 CATTGAAGATATAGCTTTCTCAAGCAACATTGGACAGCTTTTCTAGAAGCTCACTAA 4829
QY 5852 AGAACAGAGGAGGAAGATATAGTTGTGGAAGCTTTTAAACAGCACACTTTTGGTGGGAACG 5911
DB 4830 AGAACAGAGGAGGAAGATATAGTTGTGGAAGCTTTTAAACAGCACACTTTTGGTGGGAACG 4889
QY 5912 AACACAGAGATAGAGTAGTATTTCGA 5939
DB 4890 AACACAGAGATAGAGTAGTATTTCGA 4917

RESULT 8
AAD37619
ID AAD37619 standard; cDNA; 4785 BP.
XX
AC AAD37619;
DT 10-SEP-2002 (first entry)
XX
DE Human transporter protein cDNA #2.
XX
KW Human; novel human protein; NHP; transporter protein; mental disorder;
KW cancer; gene therapy; drug screening; nutraceutical application; gene;
KW cosmetic application; polymorphism; ss.
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FH Key Location/Qualifiers
FT CDS 1..4785
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FT /transl_except= (pos:2494..2496, aa:Ser)
FT /transl_except= (pos:2878..2880, aa:Val)
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FT 2494
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FT /*tag= c
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FT 2878
FT misc_feature
FT /*tag= d
FT /note= "This degenerate base represents a
FT polymorphic site"
FT
FT WO200231147-A2.
XX
XX 18-APR-2002.
XX
XX 04-OCT-2001; 2001WO-US31113.
XX
XX 10-OCT-2000; 2000US-239629P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Hu Y, Nepomnichy B;
XX
XX WPI; 2002-452347/48.
XX
XX P-PSDB; AAE23657.
XX
```

Novel nucleic acid molecule encoding novel human proteins, useful for therapeutic, diagnostic and pharmacogenomic applications - Claim 1; Page 39-41; 46pp; English.

The present sequence is a cDNA coding for novel human protein (NHP), human transporter protein. NHPs shares structural similarity with the mammalian ATP-binding cassette (ABC) transporters and multidrug resistance transporters. NHP polynucleotides are useful for the therapeutic, diagnostic and pharmacogenomic applications. They are used for detecting and treating mental disorders and cancers. They are also used in gene therapy. NHP polypeptides are useful for diagnosis, drug screening, clinical trial monitoring, treatment of diseases and disorders, and cosmetic or nutraceutical applications.

Sequence 4785 BP; 1489 A; 807 C; 917 G; 1568 T; 4 other;

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Query Match 72.9%; Score 4754.8; DB 24; Length 4785;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4756; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1011 ATGTCCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACAGACACTTCTACTGAAG 1070
DB 1 ATGTCCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACAGACACTTCTACTGAAG 60

QY 1071 AATTACTTAAATTAATGCAGAACCAAAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTA 1130
DB 61 AATTACTTAAATTAATGCAGAACCAAAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTA 120

QY 1131 TTTTCTTAAATTTGGTTAAATTAATTAATAGATGATGATCCAAATAAGAAATATGAAGAA 1190
DB 121 TTTTCTTAAATTTGGTTAAATTAATTAATAGATGATGATCCAAATAAGAAATATGAAGAA 180

QY 1191 GTGCTTAAATAGAACTCAATCTATGGACAACTTTACTCTTTCTTAATCTTATCTTGGGA 1250
DB 181 GTGCTTAAATAGAACTCAATCTATGGACAACTTTACTCTTTCTTAATCTTATCTTGGGA 240

QY 1251 TATACCTCCAGTGACTAATATTAACAGCAGCATCATGCAGAAAAGTGTCTACTGATCATCTA 1310
DB 241 TATACCTCCAGTGACTAATATTAACAGCAGCATCATGCAGAAAAGTGTCTACTGATCATCTA 300

QY 1311 CTTGATGTCATAATTAATCTGAAGAAATATACAAATGAAAGAAATGTTTAAACATCAGTCTC 1370
DB 301 CTTGATGTCATAATTAATCTGAAGAAATATACAAATGAAAGAAATGTTTAAACATCAGTCTC 360

QY 1371 TCTAAGCCGAGCAACTTTGTAGTGTGGTTTCAAGACCTCCATGCTCTATGAACTTCGT 1430
DB 361 TCTAAGCCGAGCAACTTTGTAGTGTGGTTTCAAGACCTCCATGCTCTATGAACTTCGT 420

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DB 481 AAATCATGTGAGGCTGCTCAGTACTGCTCTCAGGTTTTCACAGTTTTCACAGCATCCATA 540

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DB 541 GATGCTGCCATTTATACAGTTTGAAGCAATGTTTCTCTTTGGAGAGCTGGAGTCAACT 600

QY 1611 AAAGCTGTTTATTATGGAGAAAGCTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTA 1670
DB 601 AAAGCTGTTTATTATGGAGAAAGCTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTA 660

QY 1671 ATTTTAAATATACCTAGTTATAGCAATTTTCACTTTTGGATATCTTTTGGCAATTCATATC 1730
DB 661 ATTTTAAATATACCTAGTTATAGCAATTTTCACTTTTGGATATCTTTTGGCAATTCATATC 720

QY 1731 GTAGCAGAAAAAGAAAAAATAAGAAATTTTAAAGATAATGGGACTTTCATGATACT 1790
DB 721 GTAGCAGAAAAAGAAAAAATAAGAAATTTTAAAGATAATGGGACTTTCATGATACT 780
```


1791 GCCTTTTGGCTTCTCCGGGTTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTT 1850
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1851 ATGGCAGTCAATGCGACAGCTTCTTGTATTTCTTCAAGTACAGCAATGTGATATTT 1910
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1021 ATTGGCCTTATGATAATCTCTATAGAAAGTTTCCCAAAATCGTTAGTGTGGCTTTTCAAT 1080
2091 CCTTCTGTCACGTACTTGTGATTTGATTTGCGACAGGTCAATGATTTAGAGATTTT 2150
1081 CCTTCTGTCACGTACTTGTGATTTGATTTGCGACAGGTCAATGATTTAGAGATTTT 1140
2151 AATGAAGGTCTTCAATTTTCAAAATTTGACTGCGAGGCCATATCTCTAAATTTATACAAAT 2210
1141 AATGAAGGTCTTCAATTTTCAAAATTTGACTGCGAGGCCATATCTCTAAATTTATACAAAT 1200
2211 ATCATGCTCACATTAATAGTATATTTCTATGTCCTCTTGGCTGCTATCTTGTATCAAGTC 2270
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2271 ATTCCAGGGAAATTTGGCTTACCGAGATCATCTTATATTTTCTGAAGCCTTCAATTTGG 2330
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2511 TCATTTGACATATATGAGGTCAGATTTACTTGGCCACAGTGGAAACAGGAAG 2570
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2691 TGTCCAGATTTAGATATACACTTTGATTTTGTGACAGTGAAGAAATTTATCAATTTTG 2750
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3001	DB	ATCCAGATCTGGAGTACCCCAATCTTTTCAAGAAATTAATCTGATATAGTATTTTAAAAATTGAG	3060
4071	QY	CTGTATTTTCAAGCAGCTTTGCTTTGGAAATCATTTGTTAATCTGGAATGTCCACCTTACTTTGGCC	4130
3061	DB	CTGTATTTTCAAGCAGCTTTGCTTTGGAAATCATTTGTTAATCTGGAATGTCCACCTTACTTTGGCC	3120
4131	QY	ATGGAAAATGCAGAGATCATAGATCAAAAGCTTATATCTCAACTTAACCTTCAGAGTCCT	4190
3121	DB	ATGGAAAATGCAGAGATCATAGATCAAAAGCTTATATCTCAACTTAACCTTCAGAGTCCT	3180
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3181	DB	TTGCCATCTGCATATTGGATTGGACAAAGCTGTGTTCATATCCCTTATTTTATCATTT	3240
4251	QY	CTTATTTTGTATGTAGGAAGCTTACTGGCAATTCATTTATGGAATATTTTTTATATCTGTA	4310
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3601	DB	TATTAATCCATGGGATAGGCTTTTCAATAGCTGTTTATATATCGCTTACCTGCAAGTGTGTAATG	3660
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3721	DB	CCCTTTTTCAGAAACCTTTCAACGAAGCTTAAATAATAGGAAGCTTCCAGAAACCAACAGAC	3780
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3901	DB	GACAAGAAAGATTTTCTTTCTTCAAGAAAAAGTAAAGAAAGTGGCACTAAATACATCTCT	3960
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3961	DB	TTCTGTGTGAAAAAAGGAGAGACTTCTAGGACTATTTGGGTCCAAATGTGCTGGCAAAAGC	4020
5031	QY	ACAATTTATTAATATCTTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTATAGGA	5090
4021	DB	ACAATTTATTAATATCTTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTATAGGA	4080

Qy	5091	GATTATTTCTTCAGAGACAAGTGAAGATGATGATTCATCTGAAGTGTATGGGTTACTGTCTCT	5150
Db	4081	GATTATTTCTTCAGAGACAAGTGAAGATGATGATTCATCTGAAGTGTATGGGTTACTGTCTCT	4140
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Db	4381	ACAGGTATGGATCCCAAGGCCAAACAGCACATGTGCGAGCAATTCGAACTGCATTTTAAA	4440
Qy	5451	AACAGAAAGCGGCTGTCTATTCTTGACACCTCAGCTATATGGAGGAGGCAGAGGCTGTCTGT	5510
Db	4441	AACAGAAAGCGGCTGTCTATTCTTGACACCTCAGCTATATGGAGGAGGCAGAGGCTGTCTGT	4500
Qy	5511	GATCGAGTAGCTATCATGTGTCTGGGCAGTTAAGATGTATCGGAAACAGTACAACATCTA	5570
Db	4501	GATCGAGTAGCTATCATGTGTCTGGGCAGTTAAGATGTATCGGAAACAGTACAACATCTA	4560
Qy	5571	AAGAGTAAATTTGGAAGAAAGGCTACTTTTTTGGAATTTAAATTTGAAGACTGGATAGAAAAC	5630
Db	4561	AAGAGTAAATTTGGAAGAAAGGCTACTTTTTTGGAATTTAAATTTGAAGACTGGATAGAAAAC	4620
Qy	5631	CTAAGAAGTAGACCGCTTCAAGAGAGAAATTCAGTATATTTTCCCAATTCGAAGCCGTCAG	5690
Db	4621	CTAAGAAGTAGACCGCTTCAAGAGAGAAATTCAGTATATTTTCCCAATTCGAAGCCGTCAG	4680
Qy	5691	GAAAGTTTTTCTCTATTTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTTCA	5750
Db	4681	GAAAGTTTTTCTCTATTTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTTCA	4740
Qy	5751	CAATCTTTTTTTTAAAGCTGGAAAGAGCT	5777
Db	4741	CAATCTTTTTTTTAAAGCTGGAAAGAGCT	4767

RESULT 9
ABZ35938
ID ABZ35938 standard; cDNA; 2481 BP.

AA
AC
ABZ35938;

XX
DT 10-FEB-2003 (first entry)

DE Human secretory polynucleotide SPTM SEO ID NO 102.

Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
 asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
 Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
 multiple sclerosis; Parkinson's disease; cell proliferative disorder;
 anti-inflammatory; immunosuppressive; neuroprotective; neurologic;
 neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;
 antipsoriatic; antianemic; anti-HIV; human immunodeficiency virus;
 secretory polynucleotide; secretory protein; gene; ss.

XX Homo sapiens.

XX

PN WO200283876-A2.

 \mathbb{Y}

PD 24-OCT-2002.
XX 27-MAR-2002; 2002WO-US09921.
XX 29-MAR-2001; 2001US-280067P.
PR 29-MAR-2001; 2001US-280068P.
PR 16-MAY-2001; 2001US-291280P.
PR 17-MAY-2001; 2001US-291829P.
PR 17-MAY-2001; 2001US-291849P.
PR 19-JUN-2001; 2001US-299428P.
PR 20-JUN-2001; 2001US-299776P.
PR 20-JUN-2001; 2001US-300001P.
XX (INCY-) INCYTE GENOMICS INC.
XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GB, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin BH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RX, Urashka MB;
XX WPI; 2003-075543/07.
DR P-PSDB; ABP75491.
XX New human secretory proteins and polynucleotides, useful for
PT diagnosing, treating or preventing autoimmune/inflammatory disorders
PT (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell
PT proliferations, or cancers -
XX Claim 1; SEQ ID NO 102; 458pp + Sequence Listing; English.
XX The invention relates to a secretory polynucleotide (designated sptm)
CC comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a
CC naturally occurring polynucleotide sequence at least 90 % identical to
CC the polynucleotide sequence, a polynucleotide complementary to them or an
CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
CC treating, preventing or diagnosing a disease or condition associated with
CC the expression of functional sptm. These are particularly useful for
CC diagnosing, treating or preventing autoimmune/inflammatory disorders
CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
CC psoriasis, polycythemia vera, or cancers including adenocarcinoma, brain,
CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the
CC breast, cervix or prostate).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 2481 BP; 662 A; 452 C; 477 G; 889 T; 1 other;
Query Match 36.5%; Score 2378.8; DB 25; Length 2481;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2391; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AAAATGTTGATATTTCTCTTAGCAGGCTGTCACACGAGTTAGGTTCCAGGTCATAGTTT 60
DB 87 AAAATGTTGATATTTCTCTTAGCAGGCTGTCACACGAGTTAGGTTCCAGGTCATAGTTT 146
QY 61 CTACCCACATCTTTGACGTAGTGTGCTATTTAGTTTATTTTCAAAAACCTTTTGCAG 120
DB 147 CTACCCACATCTTTGACGTAGTGTGCTATTTAGTTTATTTTCAAAAACCTTTTGCAG 206
QY 121 TACCTTTTGGTCTGCTCTGTGTGTGCTCTGACAGTGAACAGTCTGGATTTGGACAGTGT 180
DB 207 TACCTTTTGGTCTGCTCTGTGTGTGCTCTGACAGTGAACAGTCTGGATTTGGACAGTGT 266
QY 181 CTGTCTGTTAGTTCAGTTTCTCAAGCCTTTGTGCACACTAATAGATTTTATGATGTC 240
DB 267 CTGTCTGTTAGTTCAGTTTCTCAAGCCTTTGTGCACACTAATAGATTTTATGATGTC 326

241 TCCAGCTTGGGAATTAATTAAGGAATTAATAAACAATTTTGTAGAGTGTCTTCTGAGCTC 300
327 TCCAGCTTGGGAATTAATTAAGGAATTAATAAACAATTTTGTAGAGTGTCTTCTGAGCTC 386
301 TCTTTCTAATTTTGTCCCTTCTACTTTTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 360
387 TCTTTCTAATTTTGTCCCTTCTACTTTTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 446
361 AGCCAGAGAGCTAGTGTGTTTATTTTCTCCATTTGTGTTTACACACTTGTGAGCTGCAACAC 420
447 AGCCAGAGAGCTAGTGTGTTTATTTTCTCCATTTGTGTTTACACACTTGTGAGCTGCAACAC 506
421 CATATCCAGGGCCCAATGCTAGGAGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
507 CATATCCAGGGCCCAATGCTAGGAGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566
481 TCTTCAACAGATGTTCCATTTGAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
567 TCTTCAACAGATGTTCCATTTGAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 626
541 GCACCTAGGCTTTGTTACTGTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
627 GCACCTAGGCTTTGTTACTGTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 686
601 ATACAGAGAGATTCAG 660
687 ATACAGAGAGATTCAG 746
661 AGACCTCCTTGGCCCATTTCTCAATTCAGAGCTGAGCTTCTTCTGAGCTGCTGCTGCTGCT 720
747 AAGACTTCCCTTGGCCCATTTCTCAATTCAGAGCTGAGCTTCTTCTGAGCTGCTGCTGCTG 806
721 GGGCGGTTTGGGAGATACCAAG 780
807 GGGCGGTTTGGGAGATACCAAG 866
781 ATCTGGTCTACCCATTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
867 ATCTGGTCTACCCATTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 926
841 CCATGCTATCTGTCAGTTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
927 CCATGCTATCTGTCAGTTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 986
901 CTGGGACTGAAACAGCTGCTTATTTTGGCGTTTAAATAATTAACATGAGCTTACTGCTGCTG 960
987 CTGGGACTGAAACAGCTGCTTATTTTGGCGTTTAAATAATTAACATGAGCTTACTGCTGCTG 1046
961 TCCGGGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 1019
1047 TCCGGGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 1106
1020 GCAATTAGGAGGTAGGAGTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1079
1107 GCAATTAGGAGGTAGGAGTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1166
1080 ATTAATTCAGAACCAAAAGAGAGTGTCTCAGGAGAAATTTCTTTTCCACTATTTTCTTTT 1139
1167 ATTAATTCAGAACCAAAAGAGAGTGTCTCAGGAGAAATTTCTTTTCCACTATTTTCTTTT 1226
1140 TTTTGTGTTTAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1199
1227 TTTTGTGTTTAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1286
1200 ATAGAACTCAATCTTATGGAAGAGTTTACTCTTTTCTAATCTAATCTTGTGATGATGATGAT 1259
1287 ATAGAACTCAATCTTATGGAAGAGTTTACTCTTTTCTAATCTAATCTTGTGATGATGATGAT 1346
1260 GTGACTTAATTAATTAATGAGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1319
1347 GTGACTTAATTAATTAATGAGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1406
1320 ATAATTAATTAATTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1379

Db 1407 ATAAATTACTGAAGATATACAAATGAAAAAGAAATGTTAACTCCAGTCTCTCTAAAGCCG 1466
QY 1380 AGCAACTTTCTAGTGTGGTTTTCAAGAGCTCCATGTCCTATGAACCTTCGTTTTTTTCT 1439
Db 1467 AGCAACTTTCTAGTGTGGTTTTCAAGAGCTCCATGTCCTATGAACCTTCGTTTTTTTCT 1526
QY 1440 GATATGATTCAGATATCTTCTATTATATATGATGATCAAGAGCTGGCTGTTCAAAATCATGT 1499
Db 1527 GATATGATTCAGATATCTTCTATTATATGATGATCAAGAGCTGGCTGTTCAAAATCATGT 1586
QY 1500 GAGGCTGCTCAGTACTGCTCCTCAGTTTCAAGTTTCAAGCATCCATAGATGCTGCC 1559
Db 1587 GAGGCTGCTCAGTACTGCTCCTCAGTTTCAAGTTTCAAGCATCCATAGATGCTGCC 1646
QY 1560 ATTATACAGTTTGAAGCAATGTTCTCTTTTGAAGGAGCTGGAGTCAAGTAAAGCTGTT 1619
Db 1647 ATTATACAGTTTGAAGCAATGTTCTCTTTTGAAGGAGCTGGAGTCAAGTAAAGCTGTT 1706
QY 1620 ATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTAATTTTAATA 1679
Db 1707 ATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTAATTTTAATA 1766
QY 1680 TACTAGTTATAGCATTTTCACTTTTGGATACCTTTTGGCAATTCATATCGTAGCAGAA 1739
Db 1767 TACTAGTTATAGCATTTTCACTTTTGGATACCTTTTGGCAATTCATATCGTAGCAGAA 1826
QY 1740 AAAGAAAAAATAAAGAAATTTTAAAGATATGAGGAGCTTCATGATACCTGCTTTTGG 1799
Db 1827 AAAGAAAAAATAAAGAAATTTTAAAGATATGAGGAGCTTCATGATACCTGCTTTTGG 1886
QY 1800 CTTTCTCGGTTCTCTATATACAAAGTTTAAATTTTCTATGTCCTTTCTTATGGCAGTC 1859
Db 1887 CTTTCTCGGTTCTCTATATACAAAGTTTAAATTTTCTATGTCCTTTCTTATGGCAGTC 1946
QY 1860 ATTGCGACAGCTTTTGGTTATTTCTCAAAGTAGCAGCATTTGTGATATTTCTGTTTTT 1919
Db 1947 ATTGCGACAGCTTTTGGTTATTTCTCAAAGTAGCAGCATTTGTGATATTTCTGTTTTT 2006
QY 1920 TTCTTTATGATATCATCTGATTTTGTGCTTTTAAATGCTGACACTCTTTTAAATAA 1979
Db 2007 TTCTTTATGATATCATCTGATTTTGTGCTTTTAAATGCTGACACTCTTTTAAATAA 2066
QY 1980 TCAAAACATGCGGAATAGTTGAATTTTGTACTGTGCTTTTGGATTTATGGCCTT 2039
Db 2067 TCAAAACATGCGGAATAGTTGAATTTTGTACTGTGCTTTTGGATTTATGGCCTT 2126
QY 2040 ATGATTAATCTCATAGAAAGTTTCCAAATCGTTAGTGTGGCTTTTCAGTCTCTTTCTGT 2099
Db 2127 ATGATTAATCTCATAGAAAGTTTCCAAATCGTTAGTGTGGCTTTTCAGTCTCTTTCTGT 2186
QY 2100 CACTGTACTTTTGTGATTTGATTTGACAGGTCATGCTATGATTTAGAGATTTTATGAAGT 2159
Db 2187 CACTGTACTTTTGTGATTTGATTTGACAGGTCATGCTATGATTTAGAGATTTTATGAAGT 2246
QY 2160 GCTTCATTTTCAAATTTGACTGCGAGGCCATATCTCTAATTTATCAATTTATCATGCTC 2219
Db 2247 GCTTCATTTTCAAATTTGACTGCGAGGCCATATCTCTAATTTATCAATTTATCATGCTC 2306
QY 2220 ACATTTAATAGTATATTTCTATGTCCTTTGGCTGTCTATCTTGATCAAGTCATTTCCAGGG 2279
Db 2307 ACATTTAATAGTATATTTCTATGTCCTTTGGCTGTCTATCTTGATCAAGTCATTTCCAGGG 2366
QY 2280 GAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAGCCCTTCATATGGTCAAGAGT 2339
Db 2367 GAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAGCCCTTCATATNGGTCAGAGAGC 2426
QY 2340 AAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAAATGCAATATTTAGTTTTTA 2394
Db 2427 AAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAAATGCAATATTTAGTTTTTA 2481

ABK35707
ID ABK35707 standard; cDNA; 3928 BP.
XX
AC ABK35707;
XX
DT 08-MAY-2002 (first entry)
XX
DE cDNA sequence #98 encoding novel human secreted protein.
XX
DE Human secreted protein; hyperproliferative disorder; autoimmune disorder;
XX immune deficiency disorder; blood disorder; inflammatory disorder;
XX KW infectious disorder; allergic condition; neurodegenerative disorder;
XX KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
XX KW tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
XX OS Homo sapiens.
XX
XX WO200177289-A2.
XX
XX 18-OCT-2001.
XX
XX 29-MAR-2001; 2001WO-US10232.
XX
XX 06-APR-2000; 2000US-195605P.
XX
XX (GEMY) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
XX Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;
XX Clark HF, Fachtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;
XX WPI; 2002-179322/23.
XX
XX Six hundred and twenty three polynucleotides derived from a variety of
XX human tissue sources which encode secreted proteins, useful for
XX treating immune deficiencies and disorders such as autoimmune disorders
XX
XX Claim 1; Page 127-128; 393pp; English.
XX
XX The present invention relates to the isolation of novel cDNA sequences
XX which encode human secreted proteins. The cDNA sequences have been
XX derived from a variety of human tissues. The invention also provides
XX a method for producing proteins from these polynucleotide sequences.
XX The proteins are useful for identifying compounds that modulate their
XX activity and production. The sequences of the invention are
XX useful for treating diseases such as hyperproliferative disorders
XX (e.g. cancer), immune deficiency disorders (e.g. severe combined
XX immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
XX sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
XX disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),
XX allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.
XX Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.
XX haemophilia), and tumours. The polynucleotide sequences of the
XX invention are also useful in gene therapy. ABK35610-ABK36232 represent
XX the cDNA sequences of the invention that encode for novel human
XX secreted proteins.
SQ Sequence 3928 BP; 1139 A; 681 C; 799 G; 1309 T; 0 other;
Query Match 27.4%; Score 1789.4; DB 24; Length 3928;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1833; Conservative 0; Mismatches 1; Indels 33; Gaps 1;
QY 1941 GATATTTTGTCTTAAATGTCACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTT 2000
Db 1 GATATTTTGTCTTAAATGTCACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTT 60
QY 2001 GAATTTTGTCTTAAATGTCACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTT 2060
Db 61 GAATTTTGTCTTAAATGTCACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTT 120
QY 2061 TTTCCCAAAATCGTTAGTGTGGCTTTTTCAGTCTCTTCTGTCTACTGTCTTTGTGTTGGT 2120

121 TTTCCCAATCGTAGTGGCTTTTCAGTCCCTTCTGTCACGTGACTTTTGTGATTGGT 180
12121 ATTGCACAGTCATGCAATTTAGAGATTTTAATGAAGGTGCTTCATTTTCAAAATTTGACT 2180
181 ATTGCACAGTCATGCAATTTAGAGATTTTAATGAAGGTGCTTCATTTTCAAAATTTGACT 240
2181 GCAGGCCCATATCCTCTAAATTTACAAATTTATCATCTCATCTCACTTAATAGTATATTCTAT 2240
241 GCAGGCCCATATCCTCTAAATTTACAAATTTATCATCTCATCTTAATAGTATATTCTAT 300
2241 GTCTCTTGTGCTGTATCTTTGATCAAGTCATTTCCAGGGGAATTTGGCTTACGGAGATCA 2300
301 GTCTCTTGTGCTGTATCTTTGATCAAGTCATTTCCAGGGGAATTTGGCTTACGGAGATCA 360
2301 TCTTTATATTTTCTGAAGCCTTCATATTTGTCAAGAGTAAGAAATTTATGAGGAGTTA 2360
361 TCTTTATATTTTCTGAAGCCTTCATATTTGTCAAGAGTAAGAAATTTATGAGGAGTTA 420
2361 TCAGAGGCCAATGTTAATGAAATATTTAGTTTGTGAAATTTATGAGCCAGTTCTTCTCA 2420
421 TCAGAGGCCAATGTTAATGAAATATTTAGTTTGTGAAATTTATGAGCCAGTTCTTCTCA 480
2421 GAATTTGTAGCAAAAGCAATTAAGAAATTTAGTGGTATTCAGAAAGACATACAGAAAGAAG 2480
481 GAATTTGTAGCAAAAGCAATTAAGAAATTTAGTGGTATTCAGAAAGACATACAGAAAGAAG 540
2481 GGTGAAATGTGAGGCTTTGAGAAATTTGTCTATTTGACATATGAGGGTCAAGTACT 2540
541 GGTGAAATGTGAGGCTTTGAGAAATTTGTCTATTTGACATATGAGGGTCAAGTACT 600
2541 GCCTTACTTGGCCACAGTGAACAGGAAAGAGTACATTTGATGAATTTCTTGTGACATC 2600
601 GCCTTACTTGGCCACAGTGAACAGGAAAGAGTACATTTGATGAATTTCTTGTGACATC 660
2601 TGCCCACTTCTGATGGTTTGCATCTATATATGACACAGAGTCTCAGAAATAGATGAA 2660
661 TGCCCACTTCTGATGGTTTGCATCTATATATGACACAGAGTCTCAGAAATAGATGAA 720
2661 ATGTTGAAGCAAGAAATTTGATGGATTTGTCACAGTTAGATATACATTTGATGTT 2720
721 ATGTTGAAGCAAGAAATTTGATGGATTTGTCACAGTTAGATATACATTTGATGTT 780
2721 TTGACAGTACAGAAATTTATCAATTTTGGCTTCAATCAAGGATACCCAGCAACAAT 2780
781 TTGACAGTACAGAAATTTATCAATTTTGGCTTCAATCAAGGATACCCAGCAACAAT 840
2781 ATATAACAAGAGTGCAGAAAGTTTACTAGATTTAGACATGCAGACTATCAAGAATAAC 2840
841 ATATAACAAGAGTGCAGAAAGTTTACTAGATTTAGACATGCAGACTATCAAGAATAAC 900
2841 CAAGCTAAAAATTTAAGTGGTGCAGAAAGAGCTGCATTTAGGAATTCGTGTTCTT 2900
901 CAAGCTAAAAATTTAAGTGGTGCAGAAAGAGCTGCATTTAGGAATTCGTGTTCTT 960
2901 GGGAAACCAAGTACTGCTGATAGTGAACCAAGCTGGAATGACCCCTGTTCTCGA 2960
961 GGGAAACCAAGTACTGCTGATAGTGAACCAAGCTGGAATGACCCCTGTTCTCGA 1020
2961 CATATTGTATGGAATCTTTTAAATAACAGAAAGCCCAATCGGGTGACAGTGTTCAGTACT 3020
1021 CATATTGTATGGAATCTTTTAAATAACAGAAAGCCCAATCGGGTGACAGTGTTCAGTACT 1080
3021 CATTTTATGATGAGTGCATCTTTTGCATAGTGAAGAGCTGTGATATCAAGAAGATG 3080
1081 CATTTTATGATGAGTGCATCTTTTGCATAGTGAAGAGCTGTGATATCAAGAAGATG 1140
3081 CTGAAATGTGTTGTTCTTCAATGTTCTCAAAAGTAAATCGGGGATCGGCTACCCGCTG 3140
1141 CTGAAATGTGTTGTTCTTCAATGTTCTCAAAAGTAAATCGGGGATCGGCTACCCGCTG 1200
3141 AGCATGTACATAGACAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAACAT 3200

Db 1201 AGCATGTACATAGACAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAACAT 1260
Qy 3201 ATACCTGGAGCTACTTTTATTACAACAGAAATGACAAACATTTGTGTATAGCTTGGCTTTTC 3260
Db 1261 ATACCTGGAGCTACTTTTATTACAACAGAAATGACAAACATTTGTGTATAGCTTGGCTTTTC 1320
Qy 3261 AAGGACATGGACAAATTTTTCAG-----GTTTG 3287
1321 AAGGACATGGACAAATTTTTCAGAAATGCTTGTATAGACAAAGGATGTTATTGATGTTTG 1380
3288 TTTTCTGCCCTTAGACAGTCATTTCAAATTTGGTGTCTATTTCTTATGGTGTTCATGAGC 3347
1381 TTTTCTGCCCTTAGACAGTCATTTCAAATTTGGTGTCTATTTCTTATGGTGTTCATGAGC 1440
3348 ACTTTTGAAGAGCTATTTTAAAGCTAGAAAGTTGAAGCAGAAATGACCAAGCAGATTAT 3407
1441 ACTTTTGAAGAGCTATTTTAAAGCTAGAAAGTTGAAGCAGAAATGACCAAGCAGATTAT 1500
3408 AGTGTATTTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGTGATGAAATG 3467
1501 AGTGTATTTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGTGATGAAATG 1560
3468 GAACAGAGCTTACTTATTTCTTTTCTGAAAACCAAGGCTTCTTAGTGAGCACCATGAGCCTT 3527
1561 GAACAGAGCTTACTTATTTCTTTTCTGAAAACCAAGGCTTCTTAGTGAGCACCATGAGCCTT 1620
3528 TGGAAACCAACAGATGATACAAATAGCAAGTTTCAATTTCTTTTACCTTGAACGTCGAAAGT 3587
1621 TGGAAACCAACAGATGATACAAATAGCAAGTTTCAATTTCTTTTACCTTGAACGTCGAAAGT 1680
3588 AAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATG 3647
1681 AAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATG 1740
3648 TTTTGGTTCATCATCTCTTTTAAAAATGCTGTGGTTCCTATCAAACTTGTTCAGACTTA 3707
1741 TTTTGGTTCATCATCTCTTTTAAAAATGCTGTGGTTCCTATCAAACTTGTTCAGACTTA 1800
3708 TATTTTCTTAAACCTGGAGACAAACCATATAAACAACAAAGTCTGCTTCTTCAAAAT 3767
1801 TATTTTCTTAAACCTGGAGACAAACCATATAAACAACAAAGTCTGCTTCTTCAAAAT 1860
3768 TCTGCTG 3774
1861 TCTGCTG 1867
RESULT 11
AAS63176
ID AAS63176 standard; cdna; 1818 BP.
XX AAS63176;
AC AAS63176;
XX
DT 29-JAN-2002 (first entry)
XX
XX Human purified secretory polynucleotide #32.
DE
XX Human; purified secretory polypeptide; cell proliferative disorder; ss;
KW cancer; immune system disorder; neurological disorder; mental disorder;
KW motor neuron disorder; demyelinating disorder; neuromuscular disorder;
KW central nervous system disorder; enzyme linked immunosorbent assay;
KW ELISA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200162918-A2.
XX
PD 30-AUG-2001.
XX
XX 01-FEB-2001; 2001WO-US03465.
XX
PR 24-FEB-2000; 2000US-185215P.
PR 24-FEB-2000; 2000US-185216P.

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PR 16-MAY-2000; 2000US-205232P.
PR 17-MAY-2000; 2000US-205286P.
PR 17-MAY-2000; 2000US-205287P.
PR 17-MAY-2000; 2000US-205323P.
PR 17-MAY-2000; 2000US-205324P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC;
PI Chen A, D'ea SA, Amshew S, Dahl CR, Dam TC, Daniele SE;
PI Dufour GE, Flores V, Fong WT, Greenwalt LB, Hillman JL, Jones AL;
PI Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockreher TK, Daffo A;
PI Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W;
PI Cohen HJ, Hodgson DM, Lincoln SE;
XX
XX WPI; 2001-648217/74.
XX
XX Nucleic acids encoding secretory polypeptides, useful in genetic
PT diagnosis and therapy -
XX
XX Claim 1; Page 153-154; 237pp; English.
XX
CC Sequences AAS63145-AAS63223 represent DNA encoding purified secretory
CC polypeptides of the invention. The polypeptides and polynucleotides can
CC be used in the treatment, prevention and diagnosis of diseases associated
CC with inappropriate secretory protein expression. These diseases include
CC cell proliferative disorders such as atherosclerosis and psoriasis,
CC cancers such as leukaemia and melanoma, immune system disorders such as
CC asthma and diabetes mellitus, neurological disorders such as epilepsy and
CC Parkinson's disease, mental disorders such as schizophrenia and seasonal
CC affective disorder (SAD), motor neuron disorders such as amyotrophic
CC lateral sclerosis, demyelinating disorders such as multiple sclerosis,
CC central nervous system disorders such as mental retardation and
CC neurofibromatosis and neuromuscular disorders such as cerebral palsy and
CC muscular dystrophy. Target polynucleotides in a sample can be detected by
CC hybridising the sample with a probe sequence complementary to the target
CC polynucleotide, under conditions in which a hybridisation complex is
CC formed, and detecting the presence or absence of the complex. The
CC polypeptides may also be used as antigens in the production of antibodies
CC against secretory proteins and in assays to identify modulators of
CC protein expression and activity. The antibodies may also be used as
CC diagnostic agents for detecting the presence of the sequences of the
CC invention in samples e.g. by enzyme linked immunosorbent assay (ELISA).
XX
SQ Sequence 1818 BP; 482 A; 347 C; 362 G; 627 T; 0 other;

Query Match      26.4%; Score 1722.8; DB 22; Length 1818;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1735; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 AAAATGTTGATATTTCTCTAGCAGGCTCTCAACAGGTTAGGTTGAGTTCAGTTCATAGTTT 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 81 AAAATGTTGATATTTCTCTAGCAGGCTCTCAACAGGTTAGGTTGAGTTCAGTTCATAGTTT 140
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 CTACCCACATCTTTGAACTGATGTTCTCATTTTGTAGTTTATTTTCAAAAACCTTTTGCGAG 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 141 CTACCCACATCTTTGAACTGATGTTCTCATTTTGTAGTTTATTTTCAAAAACCTTTTGCGAG 200
QY 121 TACCTTTTGGTCTGCTTGTGTGTGCTTGTGCAAGTGAACAGTCTGGATTTGGACAGTGT 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 201 TACCTTTTGGTCTGCTTGTGTGTGCTTGTGCAAGTGAACAGTCTGGATTTGGACAGTGT 260
QY 181 CTGTCGTGTAGTTTCAAGTCTTCTCAAGCCTTTGTCACTATAGGATTTGATTTATGTATG 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 261 CTGTCGTGTAGTTTCAAGTCTTCTCAAGCCTTTGTCACTATAGGATTTGATTTATGTATG 320
QY 241 TCACAGCTTGGGAATTTATTCAGGAATTAATAAACAACCTTTTGTAGTCTTTTCTTGAGCTC 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 321 TCACAGCTTGGGAATTTATTCAGGAATTTAAACAACCTTTTGTAGTCTTTTCTTGAGCTC 380
QY 301 TCTTTCTATTGTTCCCTCTCTACTTTTGTGCTTCCCTGCTGGCTGCTTTCTATCTCTCC 360
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 381 TCTTTCTATTGTTCCCTCTCTACTTTTGTGCTTCCCTGCTGGCTGCTTTCTATCTCTCC 440
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QY 1440 GATATGATCCAGTATCTTCTATTTATATGGAATCAAGAGCTGGCTGTTCAAAATCATGT 1499
DB |||||
QY 1521 GATATGATCCAGTATCTTCTATTTATATGGAATCAAGAGCTGGCTGTTCAAAATCATGT 1580
DB |||||
QY 1500 GAGCTGCTCAGTACTGGTCTCAGGTTTTCACAGTTTTCACAGTATCCATAGATGCTGCC 1559
DB |||||
QY 1581 GAGCTGCTCAGTACTGGTCTCAGGTTTTCACAGTTTTCACAGTATCCATAGATGCTGCC 1640
DB |||||
QY 1560 ATTATACAGTTGAAGACCAATGTTCTCTTTGGAAGAGCTGGAGTCACTAAAGCTGTT 1619
DB |||||
QY 1641 ATTATACAGTTGAAGACCAATGTTCTCTTTGGAAGAGCTGGAGTCACTAAAGCTGTT 1700
DB |||||
QY 1620 ATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGAGTAAATTTTAAATA 1679
DB |||||
QY 1701 ATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGAGTAAATTTTAAATA 1760
DB |||||
QY 1680 TACCTAGTTATAGATTTTACCTTTTGGATACCTTTTGGCAATTCANATCGTAGCAG 1737
DB |||||
QY 1761 TACCTAGTTATAGATTTTACCTTTTGGATACCTTTTGGCAATTCANATCGTAGCAG 1818
DB |||||

RESULT 12
ABK35706
ID ABK35706 standard; cDNA; 1548 BP.

AC ABK35706;

DT 08-MAY-2002 (first entry)

XX cDNA sequence #97 encoding novel human secreted protein.

XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;
XX immune deficiency disorder; blood disorder; inflammatory disorder;
XX infectious disorder; allergic condition; neurodegenerative disorder;
XX liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
XX tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.

OS Homo sapiens.

XX W0200177289-A2.

XX 18-OCT-2001.

XX 29-MAR-2001; 2001WO-US10232.

XX 06-APR-2000; 2000US-195605P.

PR (GEM) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
XX Marberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;
XX Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;
XX WPI; 2002-179322/23.

XX Six hundred and twenty three polynucleotides derived from a variety of
XX human tissue sources which encode secreted proteins, useful for
XX treating immune deficiencies and disorders such as autoimmune disorders

PS Claim 1; Page 126; 393pp; English.

XX The present invention relates to the isolation of novel cDNA sequences
XX which encode human secreted proteins. The cDNA sequences have been
XX derived from a variety of human tissues. The invention also provides
XX a method for producing proteins from these polynucleotide sequences.
XX The proteins are useful for identifying compounds that modulate their
XX activity and production. The sequences of the invention are
XX useful for treating diseases such as hyperproliferative disorders
XX (e.g. cancer), immune deficiency disorders (e.g. severe combined
XX immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
XX sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
XX disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),

CC allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.
CC Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.
CC haemophilia), and tumours. The polynucleotide sequences of the
CC invention are also useful in gene therapy. ABK35610-ABK36232 represent
CC the cDNA sequences of the invention that encode for novel human
CC secreted proteins.

XX Sequence 1548 BP; 466 A; 273 C; 268 G; 541 T; 0 other;

Query Match 23.7%; Score 1543.8; DB 24; Length 1548;
Best Local Similarity 99.8%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1545; Conservative 0;

QY 3386 AGAAATTCACCAAGCAGATTTATAGTGTATTTACTCAGCAGCCACCTCGAGGAGAAATGGA 3445
DB 1 AGAAATTCACCAAGCAGATTTATAGTGTATTTACTCAGCAGCCACCTCGAGGAGAAATGGA 60

QY 3446 TTCAAAATCTTTTGATGAAATGGAACAGAGCTTACTTCTTCTGAAACCAAGGCTTC 3505
DB 61 TTCAAAATCTTTTGATGAAATGGAACAGAGCTTACTTCTTCTGAAACCAAGGCTTC 120

QY 3506 TCTAGTGAGCACCATGAGCCTTTGGAACACAGAGTATACAATAGCAAAAGTTTCATTT 3565
DB 121 TCTAGTGAGCACCATGAGCCTTTGGAACACAGAGTATACAATAGCAAAAGTTTCATTT 180

QY 3566 CTTTACCTTGAAACCTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTT 3625
DB 181 CTTTACCTTGAAACCTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTT 240

QY 3626 TTTCACAGTTCAGATTTTATGTTTGTTCATCCTCTTTTAAAAATGCTGTGCTTC 3685
DB 241 TTTCACAGTTCAGATTTTATGTTTGTTCATCCTCTTTTAAAAATGCTGTGCTTC 300

QY 3686 CATCAAACTGTTTCAGACTTATATTTCTAAAACTCGAGACCAACACATAATACAA 3745
DB 301 CATCAAACTGTTTCAGACTTATATTTCTAAAACTCGAGACCAACACATAATACAA 360

QY 3746 AACCAAGTCTGCTTCTTCAAAATTCGCTGACTCAGATATCAGTGATCTTATTAGCTTTT 3805
DB 361 AACCAAGTCTGCTTCTTCAAAATTCGCTGACTCAGATATCAGTGATCTTATTAGCTTTT 420

QY 3806 CACAAGCCAGAACATAATGTTGAGCAGATTAATGACAGTGAATGATATCGTGGCTTC 3865
DB 421 CACAAGCCAGAACATAATGTTGAGCAGATTAATGACAGTGAATGATATCGTGGCTTC 480

QY 3866 CCATAGTGGCTTTTAAATGTTGATGTCATTCAGAAAGGACTATGTTTTCAGAGCTTTT 3925
DB 481 CCATAGTGGCTTTTAAATGTTGATGTCATTCAGAAAGGACTATGTTTTCAGAGCTTTT 540

QY 3926 CAACAGTACTATGTTTATTTTCTTACCTATATTTAGTGAATATCATTAGTAATCTATCT 3985
DB 541 CAACAGTACTATGTTTATTTTCTTACCTATATTTAGTGAATATCATTAGTAATCTATCT 600

QY 3986 TTATCATTTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATCTTTTCAAGAAAT 4045
DB 601 TTATCATTTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATCTTTTCAAGAAAT 660

QY 4046 TACTGATATAGTTTAAATGTTGATGTCATTCAGAAAGGACTATGTTTTCAGAGCTTTT 4105
DB 661 TACTGATATAGTTTAAATGTTGATGTCATTCAGAAAGGACTATGTTTTCAGAGCTTTT 720

QY 4106 TACTGCAATGCCACCTTACTTTTCCATGAAATTCAGAGATCATTAAGATCAAAAGCTTA 4165
DB 721 TACTGCAATGCCACCTTACTTTTCCATGAAATTCAGAGATCATTAAGATCAAAAGCTTA 780

QY 4166 TACTCAACTTAACTTTTTCAGGCTTTTTCGCTTCTGCATATTCGATTTGGACAAAGCTTGT 4225
DB 781 TACTCAACTTAACTTTTTCAGGCTTTTTCGCTTCTGCATATTCGATTTGGACAAAGCTTGT 840

QY 4226 TGATATCCCTTATTTTATTCATTTTATGATGCTAGGAAGCTTACTGGCATTTC 4285
DB 841 TGATATCCCTTATTTTATTCATTTTATGATGCTAGGAAGCTTACTGGCATTTC 900

Qy	4286	TTATGGATTATATTTTATATCTGTAAAGTTCCTTGCTGCTGTTTTCCTTATATGGTTA	4344
Db	901	TTATGGATTATATTTTATATCTGTAAAGTTCCTTGCTGCTGTTTTCCTTATATGGTTA	960
Qy	4346	TGTTCCATCAGTTATCTGTTCTACTTATATGCTTCTTTTACCTTTAAGAAATTTTAAA	4405
Db	961	TGTTCCATCAGTTATCTGTTCTACTTATATGCTTCTTTTACCTTTAAGAAATTTTAAA	1020
Qy	4406	TACCAAGAATTTTGGTTCATTTATCTGTGGCAGCGTTCGCTTGTATTCGAATCAC	4465
Db	1021	TACCAAGAATTTTGGTTCATTTATCTGTGGCAGCGTTCGCTTGTATTCGAATCAC	1080
Qy	4466	TGAAATTAACCTTCTTTATGGGATACACAATTGCAATTTCTTCATATGCCCTTTGTAT	4525
Db	1081	TGAAATTAACCTTCTTTATGGGATACACAATTGCAATTTCTTCATATGCCCTTTGTAT	1140
Qy	4526	CATCATTCCAATCTATCCACTCTAGGTTGCTGCTGCTTCTTCATTAAGAGATTTCTTGGAA	4585
Db	1141	CATCATTCCAATCTATCCACTCTAGGTTGCTGCTGCTTCTTCATTAAGAGATTTCTTGGAA	1200
Qy	4586	GAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTGTAT	4645
Db	1201	GAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTGTAT	1260
Qy	4646	ATCGCTTTACCTGCAGTGTGTACTGTGGATTTTCTCTTACAATCTATGAGAAAAATA	4705
Db	1261	ATCGCTTTACCTGCAGTGTGTACTGTGGATTTTCTCTTACAATCTATGAGAAAAATA	1320
Qy	4706	TGGAGGCAGATCATATAGAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAGTCTAAAAA	4765
Db	1321	TGGAGGCAGATCATATAGAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAGTCTAAAAA	1380
Qy	4766	TAGGAAGCTTCCAGAACCCACAGACATGAGGATGAAGATGCAAGTCTCAAAG	4825
Db	1381	TAGGAAGCTTCCAGAACCCACAGACATGAGGATGAAGATGCAAGTCTCAAAG	1440
Qy	4826	ACTAAAGGTCAAGAGCTGATGGGTTGCCAGTGTGTGTGAGGAGAAACCATTCATTTATGGT	4885
Db	1441	ACTAAAGGTCAAGAGCTGATGGGTTGCCAGTGTGTGTGAGGAGAAACCATTCATTTATGGT	1500
Qy	4886	CAGCAATTTTCATAGAAATATGATGACAGAAAGATTTTCTTCTTTC	4933
Db	1501	CAGCAATTTTCATAGAAATATGATGACAGAAAGATTTTCTTCTTTC	1548
RESULT 13			
AAC81717			
ID	AAC81717 standard; DNA; 1506 BP.		
XX	AAC81717;		
XX	26-FEB-2001 (first entry)		
DT	Human secreted protein coding sequence SEQ ID NO: 18.		
XX			
XX	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;		
KW	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;		
KW	vulnerable; anticonvulsant; antibacterial; antifungal; antiparasitic;		
KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;		
KW	neurological disease; infection; human; secreted protein; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200061627-A1.		
XX			
PD	19-OCT-2000.		
XX			
XX	06-APR-2000; 2000MO-US09067.		
XX			
PR	09-APR-1999; 99US-0128697.		
PR	20-JAN-2000; 2000US-0176929.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		

PA	(ROSE/) ROSEN C A.				
XX					
PI	Rosen CA, Ruben SM, Komatsoulis G;				
XX					
DR	WPI; 2000-647419/62.				
DR	P-PSDB; AAB45393.				
XX					
PT	New nucleic acid molecules encoding 49 human secreted proteins for				
PT	diagnosing, preventing, treating or ameliorating medical conditions and				
PT	used as food additives or preservatives -				
XX					
PS	Claim 1; Page 429; 521pp; English.				
XX					
CC	The invention relates to the isolation of genes AAC81710-C81758 encoding				
CC	49 human secreted proteins AAB45386-B54534. The genes can be used to				
CC	generate fusion proteins by linking to the gene for the human				
CC	immunoglobulin G Fc portion (SEQID1) for increasing the stability of				
CC	the fusion protein as compared to the human protein only. The genes and				
CC	proteins are useful for preventing, ameliorating or treating medical				
CC	conditions, e.g. by protein or gene therapy. The genes are isolated				
CC	from a range of human tissues disclosed in the specification. The				
CC	nucleic acids, proteins, antibodies and (ant)agonists are useful in				
CC	the diagnosis, treatment and prevention of: (a) cancer, e.g. breast				
CC	and ovarian cancer, and other cancers of the adrenal gland, bone, bone				
CC	marrow, breast, gastrointestinal tract, liver, lung, or urogenital;				
CC	(b) immune disorders e.g. Addison's disease, allergies, autoimmune				
CC	haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's				
CC	disease, multiple sclerosis, rheumatoid arthritis and ulcerative				
CC	colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)				
CC	wound healing; (e) neurological diseases e.g. cerebral anoxia and				
CC	epilepsy; and (f) infectious diseases such as viral, bacterial, fungal				
CC	and parasitic infections.				
XX					
SQ	Sequence 1506 BP; 509 A; 218 C; 290 G; 485 T; 4 other;				
	Query Match	20.2%;	Score 1319;	DB 21;	Length 1506;
	Best Local Similarity	92.1%;	Pred. No. 8.7e-272;		
	Matches 1460;	Conservative 1;	Mismatches 4;	Indels 121;	Gaps 2;
Qy	4941	GTAAAGAAAGTGGCAATTAATACATCTCTTCTGTGTGTAAGAAAGAGAGATCTTAGGA	5000		
Db	1	GTAAAGAAAGTGGCAATTAATACATCTCTTCTGTGTGTAAGAAAGAGAGATCTTAGGA	60		
Qy	5001	CTATTGGGTCCAAATGGTGTGCAAAAGCAAAATTAATAATATTCTGGTGGTGATATT	5060		
Db	61	CTATTGGGTCCAAATGGTGTGCAAAAGCAAAATTAATAATATTCTGGTGGTGATATT	120		
Qy	5061	GAACCAACTTCAGGCCAGGTATTTTTCAGAGATTAATTTCTTCAGAGACAAGTGAAGATGAT	5120		
Db	121	GAACCAACTTCAGGCCAGGTATTTTTCAGAGATTAATTTCTTCAGAGACAAGTGAAGATGAT	180		
Qy	5121	GATTCACCTGAAGTGTATGGTTACTGTCTCAGATAAAACCCTTTGTGGCCAGATCTACACA	5180		
Db	181	GATTCACCTGAAGTGTATGGTTACTGTCTCAGATAAAACCCTTTGTGGCCAGATCTACACA	240		
Qy	5181	TTGCAGAAACATTTTGAATTTATGAGCTGTCAAAGGAATGAGTCAAGTGCATCACTAAA	5240		
Db	241	TTGCAGAAACATTTTGAATTTATGAGCTGTCAAAGGAATGAGTCAAGTGCATCACTAAA	300		
Qy	5241	GAAGTCATAAGTCGAATAACACATGCACTTTGATTTTAAAGAAACATCTTCAGAAAGCTGTA	5300		
Db	301	GAAGTCATAAGTCGAATAACACATGCACTTTGATTTTAAAGAAACATCTTCAGAAAGCTGTA	360		
Qy	5301	AGAAATACCTTCAGAGATCAAAACGAAAGTTGTGTTTGTCTCTTAAGTATGCTAGGGAAT	5360		
Db	361	AGAAATACCTTCAGAGATCAAAACGAAAGTTGTGTTTGTCTCTTAAGTATGCTAGGGAAT	420		
Qy	5361	CCTCAGATTACTTTTGTAGATGAACCATCTACAGGTATGATCCCAAGCAACAGCAC	5420		
Db	421	CCTCAGATTACTTTTGTAGATGAACCATCTACAGGTATGATCCCAAGCAACAGCAC	480		
Qy	5421	ATGTGGCGAGCAATTCGAACTGCATTTTAAAAACAGAAAGCGGGCTGCTATTCTTGACCACT	5480		

Db 481 ATGT-----484
QY 5481 CACTATATGAGGAGGAGGAGGCTGTCTGTGATCGAGTAGCTATCATGTGTCTGGCAG 5540
Db 485 -----484
QY 5541 TTAAGATGTATCGAACAGTACACATCTAAAGAGTAAATTTGGAAAAAGGCTACTTTTGG 5600
Db 485 -----GATGTATCGAACAGTACACATCTAAAGAGTAAATTTGGAAAAAGGCTACTTTTGG 540
QY 5601 GAAATTTAAATTTGAAGGACTCGATAGAAAACCTAGAACTAGACCGCTTCAAGAGAAAT 5660
Db 541 GAAATTTAAATTTGAAGGACTCGATAGAAAACCTAGAACTAGACCGCTTCAAGAGAAAT 600
QY 5661 CAGTATATTTCCCAATGCAAGCCGTCAGAAAGTTTTCTTCTATTTTGGCTTATAA 5720
Db 601 CAGTATATTTTCCCAATGCAAGCCGTCAGAAAGTTTTCTTCTATTTTGGCTTATAA 660
QY 5721 ATTCTTAAGGAAGATGTTCACTCCCTTTTCAATCTTTTTTAAGCTGGAAGAGCTAAA 5780
Db 661 ATTCTTAAGGAAGATGTTCACTCCCTTTTCAATCTTTTTTAAGCTGGAAGAGCTAAA 720
QY 5781 CATGCTTTTCCCAATGCAAGGAGTATAGCTTTTCTCAAGCAACATGGAACAGGTTTTGTA 5840
Db 721 CATGCTTTTCCCAATGCAAGGAGTATAGCTTTTCTCAAGCAACATGGAACAGGTTTTGTA 780
QY 5841 GAACTCACTAAGAACCAAGAGGAGGAGATAGTTGTGGAACCTTTAAACAGCACAT 5900
Db 781 GAACTCACTAAGAACCAAGAGGAGGAGATAGTTGTGGAACCTTTAAACAGCACAT 840
QY 5901 TGGTGGGAACCAAGAGGAGTATAGTATTTTGAATTTGTATTGTTGGCTTGCT 5960
Db 841 TGGTGGGAACCAAGAGGAGTATAGTATTTTGAATTTGTATTGTTGGCTTGCT 900
QY 5961 TACTGGGACTTCTTTCTTTTCACTTAATTTAACTTTGGTTTAAAGGTTTTTATGG 6020
Db 901 TACTGGGACTTCTTTCTTTTCACTTAATTTAACTTTGGTTTAAAGGTTTTTATGG 960
QY 6021 AATGCTTAAGGAGAACCAAGAGGAGTATAGTATTTTCAAGCTTCTTAATTTGAATG 6080
Db 961 AATGCTTAAGGAGAACCAAGAGGAGTATAGTATTTTCAAGCTTCTTAATTTGAATG 1020
QY 6081 CTGGTGGTGTGTTTGTCTTTTCTTAAATAAAGCTATGATATTAATTAAGTGAAGCTGC 6140
Db 1021 CTGGTGGTGTGTTTGTCTTTTCTTAAATAAAGCTATGATATTAATTAAGTGAAGCTGC 1080
QY 6141 ATGTTTGTATTTGAAGTATATTTGAAGTATATGTTGTTGATGCTATCTTTTCAACATCAG 6200
Db 1081 ATGTTTGTATTTGAAGTATATTTGAAGTATATGTTGTTGATGCTATCTTTTCAACATCAG 1140
QY 6201 AAACAGTGTCTTGAATTTGATTTAAAGAAATTTGAATAGTATGTTTATTTTAAAG 6260
Db 1141 AAACAGTGTCTTGAATTTGATTTAAAGAAATTTGAATAGTATGTTTATTTTAAAG 1200
QY 6261 TTATCTTTTAAAGTATGCTTCTTAAATAAGTATGTTTCAATCTTAAATAAAG 6320
Db 1201 TTATCTTTTAAAGTATGCTTCTTAAATAAGTATGTTTCAATCTTAAATAAAG 1260
QY 6321 AACTAATACATACTAATATGATAGAAAAGTATACATAAAGCAATGTTGAAAGTTTCTGCTT 6380
Db 1261 AACTAATACATACTAATATGATAGAAAAGTATACATAAAGCAATGTTGAAAGTTTCTGCTT 1320
QY 6381 CTCCTTTTAAATTTCTAATAAAGGCACTTTGAATGGAAGTTGTCATCCGTAAAGCTGAA 6440
Db 1321 CTCCTTTTAAATTTCTAATAAAGGCACTTTGAATGGAAGTTGTCATCCGTAAAGCTGAA 1380
QY 6441 GTGTAAAGCACTAGGAAATCTCAATATAGATTTTGAAGAAAGTTATATCCACT-AGGTGG 6499
Db 1381 GTGTAAAGCACTAGGAAATCTCAATATAGATTTTGAAGAAAGTTATATCCACTAAGGTGG 1440
QY 6500 CAGTCATTGTATCAATAAAGTGAAT 6525
Db 1441 CAGTCATTGTATCAATAAAGTGAAT 1466

RESULT 14
ABN96909
ID ABN96909 standard; DNA; 1346 BP.
XX
AC ABN96909;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #3407 used to diagnose liver cancer.
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX WO200229103-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US30589.
XX
PR 02-OCT-2000; 2000US-237054P.
XX
(GENE-) GENE LOGIC INC.
PA Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
PI WPI; 2002-426119/45.
XX
DR Diagnosing and detecting the progression of liver cancer.
XX hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample
XX
PS Claim 1; SEQ ID NO 3407; 298pp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1346 BP; 451 A; 206 C; 290 G; 395 T; 4 other;

Query Match 18.1%; Score 1182; DB 24; Length 1346;
Best Local Similarity 96.5%; Pred. No. 1.5e-242;
Matches 1306; Conservative 0; Mismatches 29; Indels 19; Gaps 9;

QY 4786 CAGCAATCAGATGAGATGAAGATGTCAGAGCTGAAAGACTTAAAGGTCAGAGCTGA 4845
Db 1 CAGCAATCAGATGAGATGAGATGTCAGAGCTGAAAGACTTAAAGGTCAGAGCTGA 60
QY 4846 TGGTTTGCAGTGTGTGTGAGGAAACCATCCATTATGTCAGCAATTTGCATAAAGAT 4905
Db 61 TGGTTTGCAGTGTGTGTGAGGAAACCATCCATTATGTCAGCAATTTGCATAAAGAT 120
QY 4906 ATGATGACAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAGTGGCAACTAAATACA 4965
Db 121 ATGATGACAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAGTGGCAACTAAATACA 180

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Qy 4966 TCTCTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAATGGTGTGGCA 5025
Db 181 TCTCTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAATGGTGTGGCA 240
Qy 5026 AAGCACAATTAATAATTTCTGGTTGGTGATATTGAACCACTTCAGGCCAGGTATTTT 5085
Db 241 AAGCACAATTAATAATTTCTGGTTAGTGATATTGAACCACTTCAGGCCAGGTATTTT 300
Qy 5086 TAGGAGATTAATTTCTCAGACAGCAAGTGAAGATGATGATTCACCTGAAGTGTATGGTTACT 5145
Db 301 TAGGAGATTAATTTCTCAGACAGCAAGTGAAGATGATGATTCACCTGAAGTGTATGGTTACT 360
Qy 5146 GTCTCAGATAAACCCTTTGTGGCCAGATACATTCAGCAGGAACAATTTTGAATTTATG 5205
Db 361 GTCTCAGATAAACCCTTTGTGGCCAGATACATTCAGCAGGAACAATTTTGAATTTATG 420
Qy 5206 GAGCTGTCAAGGAATCAGTGCAGTGCACATGAAGAAGTCATAAGTCGAATACACATG 5265
Db 421 GAGCTGTCAAGGAATCAGTGCAGTGCACATGAAGAAGTCATAAGTCGAATACACATG 480
Qy 5266 CACTTGATTTAAAAGAACATCTTTCAGAAAGACTGTAAAAGAACTACCTGCAGGAATCAAC 5325
Db 481 CACTTGATTTAAAAGAACATCTTTCAGAAAGACTGTAAAAGAACTACCTGCAGGAATCAAA 540
Qy 5326 GAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTAATTTCTAGATGAAC 5385
Db 541 CGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTAATTTCTAGATGAAC 600
Qy 5386 CATCTACAGTATGGATCCCAA--GCCAAACAGCATGTGGGAGCAATTCGAATGC 5443
Db 601 CATCTACAGTCTGGATCCCAAATGCCAAACATGCACATGTGGCAATTCGAATGC 660
Qy 5444 ATTTAAAACAGAAAGCGGCTGTATTTCTGACCACTCCTATATGAGGAGCAGAGGC 5503
Db 661 AT-----NNAGCGGCTGTATTTCTGACCACTCCTATATGAGGAGCAGAGGC 711
Qy 5504 TGTCTGTGATCGAGTAGCTATCATGTGTCTGGGCACTTAAGATGTATCGGAACAGTACA 5563
Db 712 TGTCTGTGATCGAGTAGCTATCATGTGTCTGGGCACTTAAGATGTATCGGAACAGTACA 771
Qy 5564 ACATCTAAGAGTAATAATTTGGAAAGGCTACTTTTGGAAATTAATTTGAA--GGACTGGA 5622
Db 772 ACATCTAAGAGTAATAATTTGGAAAG--NACTTTTGGAAATTAATTTGAAAGGACTGGA 829
Qy 5623 TAGAAACCTTAGAG--TAGACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCA 5681
Db 830 TAGAAACCTTAGAGCTAGACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCA 889
Qy 5682 AGCGTCTAGAAAGTTTCTTCTATTTTGGCTTATAAAAATTCCTAAGGAAGATGTTTCAG 5741
Db 890 AGCGTCA--GAAGTTTCTTCTATTTTGGCTTCTAANAATTAATGAAGATGTTTCAG 948
Qy 5742 TCCCTTTCAAACTTTTAAAGTGAAGAGAGCTAAAATGCTTTTGGCCATTTGAAGAA 5801
Db 949 TCCCTTTCCCAATCTTTTAAAGTGAAGAGAGCTAAAATGCT--TTTGGCCATTTGAAGAA 1007
Qy 5802 TATAGCTTTTCTCAAGCAATTTGGAACAGTTTGTAGAACTCACTAAGAACAGAG 5861
Db 1008 TATAGC--TTTCTCAAGCAATTTGGAACAGTTTGTAGAACTCACTAAGAACAGAG 1066
Qy 5862 GAGGAATATAGTTGTGAACTTTTAAACGACACTTTTGGTGGGAAACGAACACAAGAA 5921
Db 1067 GAGGAATATAGTTGTGGAACCTTTTAAACGACACTTTTGGT--GGAAACGAACACAAGAA 1125
Qy 5922 GATAGATAGTATTTTGAATTTGATTTGTTGGTCTGCTTACTGGGACTTCTTTCTTTT 5981
Db 1126 GATAGATAGTATTTTGAATTTGATTTGTTGGTCTGCTTACTGGGACTTCTTTCTTTT 1185
Qy 5982 CACTTAATTTTAACTTTGTTTAAAAAGTTTATTTGGAATGTTAACTGGAACCAAG 6041
Db 1186 CACTTAATTTTAACTTTGTTTAAAAAGTTTATTTGGAATGTTAACTGGAACCAAG 1245
Qy 6042 AAGCAGCTGAAATTTTCTAAGCTCCTTAATTAATGAAATGCTGTGTTGTTGCTTT 6101
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Db 1246 AAGCAGCTTGAATTTTCTAAGCTCCTTAATTAATGAAATGCTGTGTTGCTTTGCTT 1305
Qy 6102 TTCTTTAAATAAACAACGTATCTAATAATTAAGTGAA 6135
Db 1306 TTCTTTAAATAAACAACGTATCTAATAATTAAGTGAA 1339

RESULT 15
ABL63763
ID ABL63763 standard; DNA; 1346 BP.
XX
AC ABL63763;
XX
DT 15-MAY-2002 (first entry)
XX
DE Breast cancer related gene sequence SEQ ID NO:2100.
XX
KW Human; cancer; colon; breast; kidney; ovary; oesophagus; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
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XX (AVAL-) AVALON PHARM.
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and,
PT determining a change in expression of a gene of a signature gene set
XX
XX Claim 1; SEQ ID 2100; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophagal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.
XX
XX Sequence 1346 BP; 451 A; 206 C; 290 G; 395 T; 4 other;
XX
XX Query Match 18.1%; Score 1182; DB 24; Length 1346;
XX Best Local Similarity 96.5%; Pred. No. 1.5e-242;
XX Matches 1306; Conservative 0; Mismatches 29; Indels 19; Gaps 9;
XX
XX 4786 CAGCAATGAGGTGAGATGAGATGTCAGAGCTGAAAGACTAAAGGTCAAGAGCTGA 4845
XX 1 CAGCAATGAGGTGAGATGAGATGTCAGAGCTGAAAGACTAAAGGTCAAGAGCTGA 60
XX
XX 4846 TGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGTCAGCAATTTGTCATAAAGAAT 4905
XX . 61 TGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGTCAGCAATTTGTCATAAAGAAT 120
XX
XX 4906 ATGATGACAAAGAAAGATTTTCTTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACA 4965
XX 121 ATGATGACAAAGAAAGATTTTCTTTCAAGAAAGTAAAGAGAGTGGCAACTAAATACA 180
XX
XX 4966 TCTCTTTCTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGGCA 5025
XX 181 TCTCTTTCTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGGCA 240
XX
XX 5026 AAAGCAAAATTTAATTTCTGTTGCTGATATTGAACCAACTCAGGCCAGGTATTTT 5085
XX 241 AAAGCAAAATTTAATTTCTGTTAGTATTTGACCAAGCTTCAAGGCCAGGTATTTT 300
XX
XX 5086 TAGGAGATTTATCTTCAGAGACAAGTGAAGATGATGATTCACCTCAAGTGTATGGTTACT 5145
XX 301 TAGGAGATTTATCTTCAGAGACAAGTGAAGATGATGATTCACCTCAAGTGTATGGTTACT 360
XX
XX 5146 GTCTCTAGATAAACCCCTTTGTGGCCAGATACATGATGTCAGGAAACATTTTGAATTTATG 5205
XX 361 GTCTCTAGATAAACCCCTTTGTGGCCAGATACATGATGTCAGGAAACATTTTGAATTTATG 420
XX
XX 5206 GAGCTGTCAAGGAAGTCAAGTGCAGTGCATGAAAGAGTCAATAGTCAATTAACCATG 5265
XX 421 GAGCTGTCAAGGAAGTCAAGTGCAGTGCATGAAAGAGTCAATAGTCAATTAACCATG 480
XX
XX 5266 CACTTGATTTTAAAGAAACATCTTTCAGAGAGCTGTGAAAGAAACCTCTGCAGGAATCAAAC 5325
XX 481 CACTTGATTTTAAAGAAACATCTTTCAGAGAGCTGTGAAAGAAACCTCTGCAGGAATCAAAC 540

QY 5326 GAAAGTGTGTGTGTGTCTCTAAGTATGCTAGGAAATCCTCAGATTAATCTTGTCTAGATGAAC 5385
DB |||||
DB 541 CGAAGTGTGTGTGTGTCTCTAAGTATGCTAGGAAATCCTCAGATTAATCTTGTCTAGATGAAC 600
QY 5386 CATCTACAGGTATGATGCCAAA--GCCAAACAGACACATGTCGGAGCAATTCGAACCTGC 5443
DB |||||
DB 601 CATCTACAGGTCTGGATCCCAATGCGAAACATGCACATGTCGGATGCAATTCGAACCTGC 660
QY 5444 ATTTTAAACACAGAGCGGGTCTTATCTGACCACTCACTATATGAGGAGGCGAGAGGC 5503
DB |||||
DB 661 AT-----NNAAGCGGGTCTTATCTGACCACTCACTATATGAGGAGGCGAGAGGC 711
QY 5504 TGTCTGTGATCGAGTAGCTATCATGTGTCTGGGAGTAAAGATGATTCGGAACAGTACA 5563
DB |||||
DB 712 TGTCTGTGATCGAGTAGCTATCATGTGTCTGGGAGTAAAGATGATTCGGAACAGTACA 771
QY 5564 ACATCTAAAGAGTAAATTTGGAAGAGCTACTTTTGGAAATTAATTAATGAA--GGAAGTGA 5622
DB |||||
DB 772 ACATCTAAAGAGTAAATTTGGAAGAG--NACTTTTGGAAATTAATTAATGAAAGAGTGA 829
QY 5623 TAGAAACCTAGAAG--TAGACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCA 5681
DB |||||
DB 830 TAGAAACCTAGAAGTGAAGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCA 889
QY 5682 AGCCCTCAGGAAAGTGTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAG 5741
DB |||||
DB 890 AGCCCTCA--GAAAGTGTCTTCTATTTTGGCTTCTAAATTAATTAAGGAAGATGTTTCAG 948
QY 5742 TCCCTTTCACATCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCATTTGCAAGAA 5801
DB |||||
DB 949 TCCCTTTCACATCTTTTAAAGCTGGAAGAGCTAAACATGCT--TTTGCCATTGAAGAA 1007
QY 5802 TATAGCTTTCTCAAGCAACATTTGGAACAGCTTTTGTAGACTCACTAAAGAAACAGAG 5861
DB |||||
DB 1008 TATAGC--TTTCTCAAGCAACATTTGGAACAGCTTTTGTAGAACTCACTAAAGAAACAGAG 1066
QY 5862 GAGGAAGATTAATGTTGGAACCTTTAAACAGACACACTTTGTTGGGAACGAAACAAAGAA 5921
DB |||||
DB 1067 GAGGAAGATTAATGTTGGAACCTTTAAACAGACACACTTTGTT--GGAACGAAACAAAGAA 1125
QY 5922 GATAGAGTATGATTTGGAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5981
DB |||||
DB 1126 GATAGAGTATGATTTGGAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1185
QY 5982 CACTTAATTTTAACTTTGTTTAAAGTGTGTTTAAAGTGTGTTTAAAGTGTGTTTAAAGTGTGTT 6041
DB |||||
DB 1186 CACTTAATTTTAACTTTGTTTAAAGTGTGTTTAAAGTGTGTTTAAAGTGTGTTTAAAGTGTGTT 1245
QY 6042 AACGCACTTGAATTTTCTAAGCTCCTTAATGAAATGCTGTTGTTGTTGTTGTTGTTGTTGTT 6101
DB |||||
DB 1246 AACGCACTTGAATTTTCTAAGCTCCTTAATGAAATGCTGTTGTTGTTGTTGTTGTTGTTGTT 1305
QY 6102 TTTCTTAAATAAAGCTATGATTAATTAAGTGA 6135
DB |||||
DB 1306 TTTCTTAAATAAAGCTATGATTAATTAAGTGA 1339

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Job time : 1052 secs